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                                                                                                                                                                                                                  A heterologous gene encoding a gene product which confers trichothecene resistance can be used to transform plant cells to make them resistant to fungal infection. The transformation method is useful for preventing mycotoxin contemination of a plant, particularly a crop plant such as wheat, maize, barley or rice, and for reducing and/or preventing the growth of a fungus of the genus Fusarium that produces a trichothecene, preferably comprising a C-3 hydroxyl group, by growing transformed crop plants in an area which is moderate to severe fungal infestation.
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                                                                                                       Plant cell for preventing mycotoxin contamination of wheat, maize, barley or rice plant, comprises heterologous polynucleotide encoding gene product expressed in cell, having trichothecene resistance
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                               Dawson JL;
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Pred. No. 0;
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                             Reed JN,
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                               Salmeron JM,
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                                                                                                                                               Trichothecin 3-0-acetyltransferase gene useful as a selective marker in gene manipulations in eukaryotic host cells -
                                                                                                                                                                                                                      This invention describes a novel protein with trichothecin 3-0-acetyltransferase activity. The gene is used as a selective marker in a gene manipulation using eukaryote as the host cell. This sequence encodes the trichothecin 3-0-acetyltransferase isolated from Fusarium
                                                                                                                                                                                                                                                                                                                                                                                                                          ACCITICGAGCAAGGICTIAAGCGCTICICCGAAGCCGTCCCATGGGTCGCAGGCCAGGTC
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Pred. No. 0;
0; Mismatches
                                                                                                                                                                                          Claim 3; Page 16-18; 25pp; Japanese.
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                                                         (RIKA ) RIKAGAKU KENKYUSHO.
(YAMA/) YAMAGUCHI I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A heterologous gene encoding a gene product which confers trichothecene resistance can be used to transform plant cells to make them resistant to fungal infection. The transformation method is particularly a crop plant such as wheat, maize, barley or rice, and for reducing and/or preventing the growth of a fungus of the genus Fusarium that produces a trichothecene, preferably comprising a C-3 hydroxyl group, by growing transformed crop plants in an area which is moderate to severe fungal infestation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTTCGAGCAAGGTCTTAAAGCGCTTCTCCGAAGCCGTCCCATGGGTCGCAAGGCCAAGGTCAA
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                                                                                                                                                                                                                                                                                                                  Plant cell for preventing mycotoxin contamination of wheat, maize, barley or rice plant, comprises heterologous polynucleotide encoding gene product expressed in cell, having trichotheceme resistance
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                                                                                                                                                                                            Dawson JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1403 BP; 350 A; 397 C; 352 G; 304 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 915.6; DB 21;
Pred. No. 6.2e-281;
0; Mismatches 264;
                                                                                                                                                                                            Reed JN,
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                                                                                                                                                                                               Salmeron JM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 8; Page 46; 62pp; English.
                                                                                                                      (NOVS ) NOVARTIS AG. (NOVS ) NOVARTIS-ERFINDUNGEN
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Matches 1087; Conserv
                                                                                                                                                                                                                                                 WPI; 2000-679374,
P-PSDB; AAB03934
                                                                      11-FEB-2000;
                                            31-MAR-1999;
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                                                                                11761 GACAGGACAAGATGCAATTATTCGTCTTCTCTCCAAGGCGTGCCGCAACGAATCATTCAC
                                                                                                                 CGAAGAGAAATGACGGCCATGAACCTCGATCGCAAGACGATAGTTCCTTACCTTGAAAA
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                                              GGTAGGCCAAGATGCGGTGATCCGTCTACTCCCAAGGCGTGCCGTAACGACCCATTCAC
                                                                                                                                                    11821 cGAGGAGGAAATCTCGGCCATGAACCTCGATCGCAAGACGGTAGTCCCTCCTTGAAAA
                                                                                                                                                                                        CTATACGATTGGCCCCGAGGTAGATCATCAGATTGTCAAAGCTGATGTAGCTGGTGGAG
                                                                                                                                                                                                                         11881 CTACAAAGTTGGTCCTGAGCTAGACCACAGATCGCCAAACC---TGCGCCTGCTGGCGA
                                                                                                                                                                                                                                                              CGCTGTTCTCACGCCGGTCAGTGCAAGCTGGGCGTTCTTCACATTCAGCCCCAAGGCCAT
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                                                                                                                                                                                                                                                                                                                                                                         trichothecene resistance can be used to transform plant cells to trichothecene resistance can be used to transform plant cells to make them resistant to fungal infection. The transformation method is useful for preventing mycotoxin contamination of a plant, particularly a crop plant such as wheat, maize, barley or rice, and for reducing and/or preventing the growth of a fungus of the genus Pusarium that produces a trichothecene, preferably comprising a C-3 hydroxyl group, by growing transformed crop plants in an area which is moderate to severe fungal infestation. Plasmid pNOV1704 comprises the Zea mays ubiquitin promoter, the phosphate mannose isomorase selectable marker and the nopaline synthase termination sequence. pNOV1704 further comprises the Zea mays ubiquitin promoter operably linked to the trichothecene 3-0-acetyl transferase sequence given in GENESEQ record AAA54206 and the nos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 362
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                                                                                                                                                                                                                                                   cell for preventing mycotoxin contamination of wheat, maize, y or rice plant, comprises heterologous polynucleotide encodi product expressed in cell, having trichothecene resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 21; Length 12949;
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                                                                                                                                                                                      Dawson JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 915.6; DB 21;
Pred. No. 2.1e-280;
0; Mismatches 264;
                                                                                                                                                                                  Reed JN,
                                                                                                                          (NOVS ) NOVARTIS AG.
(NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH
                                                                                                                                                                                                                                                                                                                                             Disclosure, Page 58-62; 62pp; English
                                                                                                                                                                                  Salmeron JM,
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                                     29-MAR-2000; 2000WO-EP02769.
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11-FEB-2000; 2000US-0502852.
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                                                                                                                                                                                  Peters C,
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                                                                      31-MAR-1999;
   12-OCT-2000
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                                                            410 ATTAGCTATCGGACCTGGCATGGCCCCCAACGACCCGGAGCCTGTGTTGCTATTGCAGCT
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            GITACCIATIGGACCIGGIACIGGICCCGACGACCAAAGCCIGIAAITCIATIGCAGCI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGCTTTCAAGATACAGCTCGACACCCTCGGCCAGCTACCAGGCCTCCTTTCGATCTACAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       plant cell for preventing mycotoxin contamination of wheat, maize, barley or rice plant, comprises heterologous polynucleotide encoding gene product expressed in cell, having trichothecene resistance activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fusarium that produces a trichothecene, preferably comprising a C-3 hydroxyl group, by growing transformed crop plants in an area which is moderate to severe fungal infestation. Plasmid pAgroTRIR comprises a selectable marker operably linked to a promoter and tremminator sequence and the tricothecene resistance gene described in GENESEQ record AAA54206 behind and in frame with the Arabidopsis thaliana UBI 3 promoter and in front of and in frame with the nos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 915.6; DB 21; Length 13737;
Pred. No. 2.1e-280;
0; Mismatches 264; Indels 3;
crop protection; mycotoxin;
heterologous gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 13737 BP; 3341 A; 3442 C; 3629 G; 3325 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       thaliana UBI 3 promoter and in front polyadenylation signal.
                        fungus; wheat; maize; barley; rice;
transformation; Fusarium; ds.
   resistant;
                                                                                                                                                                                                                                                                                                                                                                                                                                          (NOVS ) NOVARTIS AG.
(NOVS ) NOVARTIS-ERFINDUNGEN VERW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Salmeron JM,
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ilarity 80.3%;
Conservative 0
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   resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peters C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-679374/66
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Matches 1087; Conserv
                                                                                                                                                                               WO200060061-A2
                                                                                                                                                                                                                                                                                               29-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                    11-FEB-2000;
         Tricothecene
                                                                                                                                                                                                                                                                                                                                                      31-MAR-1999;
                                                                                                                                                                                                                                      12-OCT-2000.
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                                                                                                                      Synthetic
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Tricothecene resistance, resistant, crop protection; mycotoxin; fungus; wheat; maize; barley; rice; heterologous gene; transformation; Fusarium; ds.
                                 Sequence encoding trichothecene resistance polypeptide.
                                                                                                                                                                                    NOVARTIS AG.
NOVARTIS-ERFINDUNGEN VERW GES MBH
                                                                                                                                                  29-MAR-2000; 2000WO-EP02769.
                                                                                                                                                               31-MAR-1999; 99US-0282995.
11-FEB-2000; 2000US-0502852.
                                                                         Saccharomyces cerevisiae.
                                                                                                                                                                                                        Peters C,
                                                                                                                                                                                                                    WPI; 2000-679374/66.
P-PSDB; AAB03936.
                                                                                                                                                                                   (NOVS ) NOVARTIS
(NOVS ) NOVARTIS-
                                                                                                                       WO200060061-A2
                   26-FEB-2001
                                                                                                                                     12-0CT-2000
       AAA54210
                                                                                                                                                                                                       Hohn IM,
                                                                                                                                                                                                                                                              activity
                                                                                                                                                                                                                                         Plant
                                                                                      Key
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Dawson JL;

Reed JN,

Salmeron JM,

/*tag= a
/product= Trichothecene resistance polypeptide

Location/Qualifiers

135 183 255 123 300 A heterologous gene encoding a gene product which confers trichochecene resistance can be used to transform plant cells to make them resistant to fungal infection. The transformation method is useful for preventing mycotoxin contemnination of a plant, particularly a crop plant such as wheat, maize, barley or rice, and for reducing and/or preventing the growth of a fungus of the genus Fusarium that produces a trichothecene, preferably comprising a C-3 hydroxyl group, by growing transformed crop plants in an area which is moderate to severe fungal infestation. CAGCTCGACCCTCGGCCAGCTACCAGGCCTCCTTTCGATCTACACCCCAAATCAGTCTC CAACTTGATATTTTGGGACAACAACCTTCGCTATACAAACTATACACTCAAATATGCTCT CTCTACCCCGTCTCTGATTCCTCTAATATCCCACTATTGTCAGCACCTTCGAGCAAGGT 196 AGCGAGGGAAACACGAGGAACTTCCTTTTATCGTCCCTTTTTGAGGACGTTCCTCGTGTTGTA GACGAAGGTAACACTGGTACCTACAGAATTGTCCCGTCAGACAAATTCCAC---TTATC 124 Archaccereraccagarcerrerecreareaceararceraaracerraacaagaga CTTGAAACATIGGCTAAAAATTTCCAGIGGCTAGCAGGAAATGTCGTAAATGAAGGTGCT CTTAAGCGCTTCTCCGAAGCCGTCCCATGGGTCGCAGGCCAGGTCAAAGCCGAGGGCATT cell for preventing mycotoxin contamination of wheat, maize, y or rice plant, comprises heterologous polynucleotide encoding product expressed in cell, having trichothecene resistance Gaps 27; 21; Length 1425; Indels Sequence 1425 BP; 431 A; 305 C; 293 G; 396 T; 0 other; Score 249.8; DB 21; Pred. No. 1.2e-68; 0; Mismatches 622; Claim 8; Page 50-51; 62pp; English. . 0 18.4%; 51.9%; Conservative Local Similarity barley or rice Best Local Simi Matches 700; 16 9/ 136 64 184 Query Match

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GGACTCCCCGAAACGTATCCAGGGTTATTAGTCAACATGACCTTTAATACAGGTTCCCTG 1020 369 420 429 480 489 ccegacaactaacerricraracercaaccaarricarareregaarrareragere 1200 GTGAAAGACCTCCGCGATGATCCTTCAGCGCCCACGATCGAGGGTATGAGAAAGGCGGGA 315 540 549 009 609 999 999 720 717 780 777 840 837 900 838 AGAATGGATGGCTCTGCACCTACCGAGTTCTGCCGTGCTGTTGATGCTCGACGGCAATG 897 GGTGTCTCGAACAACTACCCAGGCCTTCTTCAAAACATGACCTACCACAACTCGACCATC 957 361 TITCCTATCTACATGTTAGACGAAAAGACTTTTGCGCCTTGCATGACTATCAATCCACCT 370 ATTGGACCTGGTACTGGTCCCGACGACCAAAGCCTGTAATTCTATTGCAGCTCAACTTC GGAAACACTATAGGTATGGCCCCAAGAGTGGCCCTGTATTTGCAGTTCAAGCAAACTTT ATCAAGGGGGACTCATCCTCACTGTCAACGGACAGGACGGTGCTATGGATATGGTAGGC GAACCCGACACCCTAGTTCATGAATAGTGGAAACCTCTAGAAATACAAGTGGAGAG GAAAAGGAACAGTCTTCTTCGAACTCTACTTGGGCTTATGTTGAATTTTCTGCTATC TCATTGCAGAATCTGAGGATTTTGGCAATGCAGACATGTACTTCTGGCACAAAATTTGTC rcacrdardararcarcacrdcrrrcarcrddaaarcadrrrcrcdadccddrraacr CAAGAIGCGGIGAICCGICTACICTCCAAGGCGIGCCGIAACGACCCAITCACCGAAGAG 541 CAGGAAAGTATCATCAACTTGCTCAATAAATCTTGCCACCAAAAACCTTTCTCTGATGAA GAAATGACGCCATGAACCTCGATCGCAAGACGATAGTTCCTTACCTTGAAAACTATACG 610 ATT---GGCCCCGAGGTAGATCATCAGATTGTCAAAGCTGATGTAGCTGGTGGTGACGCT GTTCTCACGCCGGTCAGT----GCAAGCTGGGCGTTCTTCACATTCAGCCCCAAG GCCATGTCAGAGCTCAAGGATGCTGCTACCAAGACTCTTGACGCATCAACAAAGTTCGTG 901 CGACTITAAACCAGAAACGAAAICAAAITITAGGGCGIGCIGIGGAIGITAGAAAAAGGGCIA 958 GGCGAAATCGCCAACGAGTCACTCGGCGCAACAGCATCACGCCTTCGTTCAGAACTCGAC 1021 AAAAGCTIGGATCATAAAAGTTIGGGCGTTCTTGCATCACAGATTCGCCAGGAAGCTAGAC CCCGCGAGCA-----TGCGCCAGCGAACAAGAGGTCTCGCGACGTACCTGCACAACAAC CCTAAAGTCTTCGATTTGGCCTATAATACATGCGCACTTGCTACGCTCCTTAGCCGATGC 1201 AGTICGIGGGCAAAGICAGCCIGIAIGACGIIGAITICAAICIAGGGCTIGGAAGCCC 1261 AAGAGTGTACGACGCCGCGCTTCATTTCCCTTGAGAGCCTAATATATTTTATGCCTAGA CCCGACAAGTCCAACGTATCCCTGACGCTGATGCGGACCCATCTACCAGCGTCATGCTG 1192 GAGACTGTGAGACGGCCAATCTTTGAGCCTTGAGAGCTTGATGTACTTTATGCCCAAG 1132 AGTICTIGGGCCAAGGIGGGACTCTGGGATTACGACTTGGGGCTCGGACTGGGTAAGCCC 1252 AAGCCTGATGGCGAGTTCTGTGCGGCGTTTCTCTGAGGGATGAGGATATGGACCGATTG TACCCTATGGCGATGTTTGACGAGAACATCGCGCGCCAAGGAAGACGTT 430 256 316 121 550 1018 661 718 781 778 841 196 1081 1072 1141 721 à g g g g δ δ ò à d à gg δ q à qq à 셤 à g à qq δ g à op à Пb ò qq ò g à

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analysis of the results. AAF07478 to AAF11247 represents ESTs from Fusarium venenatum; AAF11248 to AAF11853 represents ESTs from Aspergillus niger; AAF11854 to AAF14878 represents ESTs from Aspergillus oryzae; and AAF14879 to AAF15337 represents ESTs from Trichoderma reesei, which are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes a method for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. The method uses fluorescence-labeled mucleic acids isolated from the FF cells and a substrate of expressed sequence tags (EST). The ESTs are used in the methods for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. Monitoring the global expression of genes from FF cells allows the production potential of the microorganisms to be improved. New genes may be discovered, possible functions of unknown open reading frames can be identified and gene copy number variation and stability can be monitored. The expression of genes can be used to study how FF cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Monitoring differential expression of genes in filamentous fungal cells uses fluorescence-labeled nucleic acids isolated from the cells and a
                                                                                                                                                                                                                                                                                               Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesei; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     morphogenesis, recombination, metabolic or catabolic pathway engineering. Using ESTs provides several advantages over genomic or random cDNA clones including flumination of redundancy as one spot on array equals one gene or open reading frame, and organisation of the microarrays based on function of the gene products to facilitate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Olsen PB;
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Score 146.2; DB 21; Length 695; Pred. No. 8.9e-36;

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Query Match Best Local Similarity

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Abe K;
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Mismatches 225; Indels
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Mycobacterium tuberculosis; strain H37Rv; strain CDC 1551; genome; variation; epidemiology; patient treatment; epidemic monitoring; ds.
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The invention relates to evaluating strain variation within and between different populations of the tuberculosis bacterial pathogen, Mycobacterium tuberculosis or related Mycobacterium by determining the nucleotide sequence of the first strain at positions in the complete sequence of the genome that correspond to positions that differ in the nucleotide sequences of M. tuberculosis strains CDC 1551 (AAI99683) and H37Rv (AAI99682). The method is useful for evaluating strain variation of M. tuberculosis and has valuable application in the fields of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=6294328B1.
                                                                                                                                                                                                                                                                                                                                                                                                   Evaluating strain variation of Mycobacterium tuberculosis, comprises determining the nucleotide sequence of the strain at positions in the genome corresponding to positions where M. tuberculosis strains CDC 1551 and H37Rv differ -
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                                                                                                                                                                                                                  Fleischmann RD, White OR,
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                                                                                                                                                                                                                                                                                                                                                            The invention relates to a polynucleotide having any of 6006 specific sequences (ABZ50888-ABZ56833), which are expressed by a fungus under specific culture conditions including one or more of eutrophic, olid, early germination, alkaline, high temperature, low temperature or maltose culture or polynucleotides stringently hybridising to these sequences. The polynucleotides are useful for monitoring the progress of fermentation and the growth conditions of a fungus, especially of Aspergillus oryzae which is widely used in industrial fermentation. Also monitoring for fungal contamination.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1096 ACGCTGATGCGGACCCATCTACCAGCGTCATGCTGAGTTCTTGGGCCAAGGTGGGACTC 1155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          281
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                                                                                        Detection of expression of specific Aspergillus genes for monitoring the fermentation and growth conditions of the fungus, using DNA probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1036 CGAACAAGAGGICICGCGACGIACCIGCACAACAACCCCGGACAAGICCAACGIAICCCIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            282 GCTGTCTCGTTACAGGAGGATATGGCGCGGTTGGCGGCGGATGAAGAGTTTACGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      222 ACTCCGGTTGAAGGGTTGATTTTTATTTCATGCCCAAGAGGTCTGATGGCGAGATTGCTGTT
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                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 3930; 48pp + Sequence Listing; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches 128; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 482 BP; 131 A; 109 C; 115 G; 127 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TATGCGCAGTACGTTGGTTAG 1356
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WPI; 2003-046817/04
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4219416 TCGAGGAGGTTCGCGCCCCCACTCGACGAAGCCACCACTACGGCTACGCGATATCC 4219475
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                                                                                                                                                                                                                                                                                                4219536 ACCGGCTTACCCTGCCGTTCAACGAGGACGCCGTCGGCCCGACGCCGAGTTGCGCATTG 4219595
                                                                                                                                                                                                                                                            ACAAGTCCAACGTATCCCTGACGGCTGATGCGGACCCATCTACCAGCGTCATGCTGAGTT 1135
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Sequence 4403765 BP; 757105 A; 1447799 C; 1441301 G; 757371 T; 189 other;
                                                                                                           TCGGCGAAATCGCCAACGAGTCACTCGGCGCAACAGCATCACGCCTTCGTTCAGAACTCG
                                                                                                                                                                                   1016 ACCCGGGAGCATGCGCCAGCGAACAAGAGGTCTCGCGACGTACCTGCACAACAACCCG
                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium tuberculosis; strain H37Rv; strain CDC 1551; genome; variation; epidemiology; patient treatment; epidemic monitoring; ds
                                        DB 22; Length 4403765;
                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium tuberculosis strain H37Rv genome SEQ ID NO 1.
                                    Score 39.8; DB 22; Length
Pred. No. 8.4;
0; Mismatches 102; Indels
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                                                                                                                                                                                                                                                                                                                                     CTTGGGCCAAGGTGGGACTCTGG 1158
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                                    2.9%;
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                                                   Local Similarity 49.8
hes 101; Conservative
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                                    Query Match
                                                                         Matches
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Mizutani M;

H

Kusumi

Fukui Y,

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Vectors containing DNA fragments encoding proteins of plant origin with aromatic acyl transferase activity may be used to transform plants which produce anthocyanin pigments. The aromatic acyl transferase acylates the pigments in the flower resulting in colour tone changes and allowing new colourations to be produced. Six specific DNA sequences encoding aromatic acyl transferase from different plants are described in AAI37308-T37313.
                                                                                                                                                                                                                                                                                                                                                                                                                                DNA coding for aromatic acyl transferase - for transforming plants which produce anthocyanin pigments and thus altering colour tone, e.g. of flowers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; Page 61-65; 94pp; Japanese.
                                                                                                                                                                                                                                                                                                            T, Fujiwara H, Fukui
Tanaka Y, Yonekura K;
                                                                                                                    96WO-JP00348.
                                                                                                                                                                 96JP-0046534.
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                         WO9625500-A1
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                                                                                                                      16-FEB-1996;
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                                                                      22-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      107;
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                                                                                                                                                                                                                                                                                                              Ashikari
                                                                                                                                                                                                                                                                                                                                     Nakao M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCGGCGAAATCGCCAACGAGTCACTCGGCGCAACAGCATCACGCCTTCGTTCAGAACTCG 1015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO
                                                                                                                                                                                                                                                                                                                                                            The invention relates to evaluating strain variation within and between different populations of the tuberculosis bacterial pathogen. Wycobacterium tuberculosis or related Mycobacterium by determining the nucleotide sequence of the first strain at positions in the complete sequence of the genome that correspond to positions that differ in the nucleotide sequences of M. tuberculosis strains CDC 1551 (AR199683) and H37Rv (AA199682). The method is useful for evaluating strain variation of M. tuberculosis and has valuable application in the fields of tuberculosis genetics, epidemiology, patient treatment and epidemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4411529 BP; 758565 A; 1449983 C; 1444602 G; 758379 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1016 ACCCCGCGAGCATGCGCCAGCGAACAAGAGGTCTCGCGACGTACCTGCACAACAACCCCG
                                                                                                                                                                                        Evaluating strain variation of Mycobacterium tuberculosis, comprises determining the nucleotide sequence of the strain at positions in the genome corresponding to positions where M. tuberculosis strains CDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
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                                                                                                                                                                                                                                                                                                                      Claim 3; SEQ ID NO 1; 3pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seqdata.uspto.gov/sequence.html?DocID=6294328B1.
                                                                                                    Venter JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 39.8; DB 22;
Pred. No. 8.4;
0; Mismatches 102;
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                                                                                                       Fraser CM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAT37310 standard; cDNA to mRNA; 1605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTTGGGCCAAGGTGGGACTCTGG 1158
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       98US-0103840.
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                                                                                                       White OR,
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                                                       (GENO-) INST GENOMIC RES
                                                                                                                                                                                                                                                                        1551 and H37Rv differ
                                                                                                                                                    WPI; 2001-647261/74.
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les 101; Conserv
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                                                                                                       RD,
       24-JUN-1998;
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                                                                                                       Fleischmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               monitoring.
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                                                                                                                                                                                                                                                                                                                                                                                    1277 ACAÁTAGGTTTGATGGAATGGTGTATTTGTACCÁAGGCAAAAATGGAGGAAGAAGCATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                GTGCGGCGCTTTCTCTGTGAGGATGAGGATATGGACCGATTGAAGGCGGATAAGGAGTGGA
                                                                                                                                                                                          1154 TCTGGGATTACGACTTTGGGCTCGGACTGGGTAAGCCCCGAGACTGTGAGACGGCCAATCT
                                                                                                                                                                                                                                                         rcaagerrhacgacgregarrrrcgargegggaaagcccagagagrergaggagregrrcga
                                                                                                                                                                                                                                                                                                                     --CCAAGAAGCCTGATGGCGAGTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, cytosine methylation, 5'-CpG-3', uracil, cytosine, diagnosis, drug, side effect, cancer, central nervous system, cardiovascular; gastrointestinal, respiratory system, single nucleotide polymorphism, SNP; cell differentiation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oligonuclectide for detecting cytosine methylation SEQ ID NO 20283.
                                                               DB 17; Length 1605;
                                                                                                                              Indels
Sequence 1605 BP; 477 A; 319 C; 375 G; 434 T; 0 other;
                                                                                                                              96;
                                                           2.7%; Score 36.4; Di
51.9%; Pred. No. 1.4;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                           1214 TIGAGCCIGITGAGAGCITGAIGIACITIAIGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1331 CCAAGTATGCGCAGTACGTTGGTTAG 1356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1397 TCATGGAAACTGCTTAATTTGCTTAG 1422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABQ33692 standard; DNA; 1459 BP.
                                                                                             ilarity 51.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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(EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-371829/40.
WO200218632-A2
                                                                                             07-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Olek A,
NAMES OF STREET OF STREET
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2.6%; Score 35.6; DB 24; Length 1459; 49.0%; Pred. No. 2.4; Sequence 1459 BP; 173 A; 200 C; 526 G; 560 T; 0 other; Query Match

1108 ccaaatricececcaacrecaacrecaacrifiacaccececececaaarececaaa 1049 200 CCCCGTCTCTGATTCCTCTCAATATCCCACTATTGTCAGCACCTTCGAGCAAGGTCTTAA 140 cacceceraaaceakaariraareteraceeceeceeriraaaaceeaaaceea 989 988 ACGAATCGAACAACCCGAAACGCGCGTCTTCCGCGAATCTAAAAACGACGAAATCGACGA 929 80 CGACACCCTCGGCCAGCTACCAGGCCTCCTTTCGATCTACACCCAAATCAGTCTCCTCTA GCGCTTCTCCGAAGCCGTCCCATGGGTCGCAGGCCAGGTCAAAGCCGAGGGCATTAGCGA Gaps 0; Indels 66 0; Mismatches 201 GGGAAACACAGGAA 214 Conservative Local Similarity wes 95; Conserv 81 Best Loca Matches 셤 g ò ð ð g

928 CCGAAAAAAACGAA 915

ABQ33693 standard; DNA; 1459 12-JUL-2002 ABQ33693; ABQ33693 ID ABQ3 XX AC ABQ2 XX DT 12-c

RESULT 13

(first entry)

Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis, drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds. Oligonucleotide for detecting cytosine methylation SEQ ID NO 20284. 01-SEP-2001; 2001WO-EP10074. 01-SEP-2000; 2000DE-1043826. 05-SEP-2000; 2000DE-1044543. (EPIG-) EPIGENOMICS AG. WO200218632-A2 07-MAR-2002 Olek A, This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-cpc-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (G) but not methylated C, to uracil, then part of the genomic Cytosine (C) but not methylated C is upont then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (DNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of the rarpeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single mucleotide polymorphisms (SNP's); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously. methylation status of many C residues to be determined simultaneously. ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA. Claim 12; 56pp + Sequence Listing; 56pp; German. Guetig D; Berlin K, the disclosure of the invention. 01-SEP-2001; 2001WO-EP10074. 01-SEP-2000; 2000DE-1043826. 05-SEP-2000; 2000DE-1044543. Piepenbrock

This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic cample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation. The method allows the methylation status of many C residues to be determined simultaneously. ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the the Atachonica of the invantion Sequence 1459 BP; 560 A; 526 C; 200 G; 173 T; 0 other; the disclosure of the invention.

81 CCCCGTCTCTGATTCCTCTCTATATCCCACTATTGTCAGCACCTTCGAGGAGGTCTTAA 140 CCAAATTCGCGCCCAACTCCGACCCCACGTTTACACCCCGGCCCCGACGAATCCCCACAC 411 CACCGCCGCGTAAACGACGAAAATTAATCTCTACCCCGCGCTTTAAAACCCGAAACGCA 471 21 GAACACCCICGGCCAGCIACCAGGCCTCCTITCGATCIACACCCAAATCAGICTCCTCIA 80 472 ACGAATCGAACAACCCGAAACGCGCGTCTTCCGCGAATCTAAAAACGACGAAATCGACGA 141 GCGCTTCTCCCAAGCCGTCCCATGGGTCGCAGGCCAGGTCAAAGCCGAGGGCATTAGCGA 412

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Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA -Gaps 0; Score 35.6; DB 24; Length 1459; Pred. No. 2.4; 0; Mismatches 99; Indels 0: 99; Indels Claim 12; 56pp + Sequence Listing; 56pp; German. Guetig Berlin K, .68; 49.0%; 201 GGGAAACACAGGAA 214 532 CCGAAAAAACGAA 545 95; Conservative Piepenbrock C, WPI; 2002-371829/40. Local Similarity Query Match Matches

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Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA
                                                                                            Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.
                                                                          Oligonucleotide for detecting cytosine methylation SEQ ID NO 1033.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1463 BP; 189 A; 200 C; 521 G; 553 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                   Claim 12; 56pp + Sequence Listing; 56pp; German.
                                                                                                                                                                                                                                                                                    Guetig D;
                                                                                                                                                                                                                                                                                     Berlin K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the disclosure of the invention.
                ABQ14442 standard; DNA; 1463 BP.
                                                                                                                                                                                                                                              2000DE-1044543.
                                                                                                                                                                                                              01-SEP-2001; 2001WO-EP10074.
                                                                                                                                                                                                                                  01-SEP-2000; 2000DE-1043826
                                                          (first entry)
                                                                                                                                                                                                                                                                                     Piepenbrock C,
                                                                                                                                                                                                                                                                (EPIG-) EPIGENOMICS AG.
                                                                                                                                                                                                                                                                                                        WPI; 2002-371829/40.
                                                                                                                                                                     WO200218632-A2.
                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                             05-SEP-2000;
                                                          12-JUL-2002
                                                                                                                                                                                          07-MAR-2002
                                      ABQ14442;
                                                                                                                                                                                                                                                                                     olek A,
RESULT 14
         ABQ14442/
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This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic cytosine (C) but not methylated C, to uracil, then part of the genomic C DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligoners and the degree of hybridisation to both classes is determined from the classes of oligomers, the degree of methylation is calculated. The method CC classes of oligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders CC of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation of cell or tissue companies of investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously.

ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the companies of the degree of cytosine methylation described in the discondent degree of cytosine methylation described in

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                                                                                   1018 ccaaatricececcaacreceaceceacerriracaeececeeeceacearecaee 959
                                                       21 CGACACCCTCGGCCAGCTACCAGGCCTCCTTTCGATCTACACCCAAATCAGTCTCCTCTA
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DB 24; Length 1463;
                           Indels
                           66
               2.4;
                             0; Mismatches
 Score 35.6;
               Pred. No.
   2.6%;
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                              95; Conservative
   Query Match
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CCCCGTCTCTGATTCCTCTAATATCCCACTATTGTCAGCACCTTCGAGCAAGGTCTTAA 140

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141 GOGCTTCTCCGAAGCCGTCCCATGGGTCGCAGGCCAGGTCAAAGCCGAGGGCATTAGCGA
                                                                                                                                                                                  drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.
                                                                                                                                                                           methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
                                                                                                                                                         Oligonucleotide for detecting cytosine methylation SEQ ID NO 1034.
                                                                                                                                                                                                                                                                                                                                                                                 Determining the degree of cytosine methylation in genomic DNA, for diagnosis and prognosis, comprises selective hybridization amplicons from chemically treated DNA
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                                                                                                      ABQ14443 standard; DNA; 1463 BP.
                                                                                                                                                                                                                                                                                                  01-SEP-2000; 2000DE-1043826.
05-SEP-2000; 2000DE-1044543.
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                                       214
                                                        838 CCGAAAAAAACGAA 825
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                                                                                                                                                                                                                                                                                                                                               Piepenbrock C,
                                        201 GGGAAACACAGGAA
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                                                                                                                                                                               Human; cytosine
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                                                                                                                          ABQ14443;
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                                                                                     RESULT 15
ABQ14443
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This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert genomic cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. DNA that contains the target C is amplified to form a labeled amplicon. DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridisation to both classes is determined from the method the degree of hybridisation to both classes is determined from the classes of oligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide colymorphism investigating cell differentiation of cell or tissue colymorphism investigating cell differentiation of cell or tissue complyation status of many C residues to be determined simultaneously.

ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the contral described in the disclosure of the invention.

Claim 12; 56pp + Sequence Listing; 56pp; German.

Sequence 1463 BP; 553 A; 521 C; 200 G; 189 T; 0 other;

Length 1463; DB 24; Score 35.6; DE Pred. No. 2.4; 2.6%; Query Match. Best Local Similarity us-10-614-954-5.rng

0; Gaps 0;

0; Mismatches 99; Indels

Matches 95; Conservative

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| Description | | 93433 | ABUUN874 Gibberell | AB009607 Gibberell | AB011417 Gibberell | AF212605 Gibberell | AF212603 Gibberell | AF212606 Gibberell | AF212607 Gibberell AF212602 Gibberell | AF212604 Gibberell | AF212582 Gibberell | AFZ1Z583 Gibberell AFZ1Z584 Gibberell | AF212585 Gibberell | AF212586 Gibberell | AF212594 Gibberell | AF212601 Gibberell | AF212595 Gibberell AF212596 Gibberell | AF212597 Gibberell | AF212598 Gibberell | AF212509 Gibberell | AF212588 Gibberell | AF212589 Gibberell | Arzzzetz Gibberell Arzzsegz Gibberell | AF212590 Gibberell | AF212591 Gibberell | AF212593 Gibberell AF212593 Gibberell | AF212614 Fusarium | AF212612 Fusarium AF212613 Fisarium | AF212611 Fusarium | | AF212610 Fusarium AF212615 Fusarium | AF212616 Fusarium | AF212617 Fusarium | AR193430 Sequence | | | linear PAT 20-APR-2002 | | | | | | |
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| SUMMARIES | 1 | AR193433 | AB000874 | AB009607 | AB011417 | AF212605 AF212608 | AF212603 | AF212606 | AF212607 AF212602 | AF212604 | AF212582 | AF212584 | AF212585 | AF21286 AF212587 | AF212594 | AF212601 | AF212595 AF212596 | AF212597 | AF212598 AF212599 | AF212600 | AF212588 | AF212589 AY222642 | AY225882 | AF212590 | AF212591 | AF212593 | AF212614 | AF212612 AF212613 | AF212611 | AF212609 | AF212610 AF212615 | AF212616 | AF212617 AF212618 | AR193430 | ALIGNMENTS | | 1356 bp | ns | 98 | | | and Salmeron, J. t transgenic plants | 5 12-FEB-2002; lifiers |
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| % Query ore Match | | 100. | 986 | 98. | 98. | 20 C | 98. | 98. | 8 8 | 98 | 97. | 97. | 1321.2 97.4 | 97. | 97 | 97. | 97. | 97. | 7.0 | 18 97. | 4 97. | 4 96 | 4 96. | . 96 . 96 . | 96. | . 96 | 92. | 8 94. | 2 94. | 93. | 92. | 6 92. | o c | 6 67. | | | | Sequence 5 AR193433 | AR193433.1 | Unknown. Unknown. | Unclassifie 1 (bases 1 | Hohn, T.M., Peters, C. and Trichothecne-Resistant | Patent: US |
| Result No. Sc | 1 | | | | | | | | | | | | 16 132 | | | | | | | | | , , , | | | | | | | | | | Π. | | | | RESULT 1 | AK193433 LOCUS | ACCESSION | VERSION KEYWORDS | SOURCE | | | JOURNAL |
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| OY 961 GAMATCGCCAACGAGTCACTCGGCGC | | 1141 | 1201 | | Db 1321 AAGGAGTGGACCAAGTATGCGCAGTP | RESULT 2 B31785 LOCUS RESULT 2 B31785 LOCUS RESULT 2 | ACCESSION E31785. VERSION E31785.1 GI:13018619 KEYWORDS JF 2000032985-A/1. SOURCE Gibberella zeae | ORGANISM Gibberella zeae ORGANISM Bukaryota; Fungi; Ascomycote Hypocreomycetidae; Hypocreal OPFERBENCE 1 (hases 1 to 1605) | AUTHORS Isamu, Y., Makoto, K., Akira, 7 IIILE Trichothecene 3-0-acetyltrar JOURNAL Patent: JP 2000032985-A 1 03 PIRATAKHI KRNKYIGHO, ISAMI YAN | COMMENT OS FURBATIUM GRANINGARUM PN JP 2000032985-A/1 PD 02-FEB-2000 DP 15-THI-1998 JP 1998200 | PR P | (C12N15/09,C12R1:77),(C12N1 C12N15/00, PC C12N5/00,(C12N15/00,C1) | FT CDS Location/Qualifier source 1, .1605 | Mol type="genomic Mol | Query Match 98.8%; Score Best Local Similarity 99.3%; Pred. Matches 1346; Conservative 0. Mi | aagatacagc |
|---|--|--|--|--|--|--|---|--|--|--|---|---|--|---|--|---|
| source 11356 / Organism="unknown" SE COUNT 319 a 385 c 349 g 303 t IGIN QUELYY MATCh Best Local Similarity 100.0%; Score 1356; DB 6; Length 1356; Best Local Similarity 100.0%; Pred. No. 0; Matches 1356; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | 1 AIGGCITICAAGAIACAGCICGACACCICGGCCAGCIACCAGGCCICCITICGAICIAC 60 | 61 ACCCAAATCAGTCTCTTACCCGTCTCTGATTCCTCTCAATATCCCACTATTGTCAGC 120 | 121 ACCTTCGAGGAAGGTCTTAAGGGCTTCTCCGAAGCCGTCCCATGGGTCGCAGGCCAGGTC 180 [| 181 AAAGCCGAGGGCATTAGCGAGGGAAACACAGGAACTTCCTTTATCGTCCCTTTTGAGGAC 240 181 AAAGCCGAGGGCATTAGCGAGGGAAACACAGGAACTTCCTTTATTGTCGTCCCTTTTGAGGAC 240 | 241 GITCCTCGTGTTGTAGTGAAAGACCTCCGCGATGATCCTTCAGCGCCCACGATCGAGGGT 300 | 301 ATGAGAAAGGGGGGATACCCTATGGCGATGTTTGACGAGAACATCATCGGGCCAAGGAAG 360 | 361 ACGITACCIATIGGACCIGGTACIGGICCCGACGACCCAAAGCCIGTAAITCTAITGCAG 420 | 421 CTCAACTTCALGAAGGGGGACTCATCCTCACTCAACGGACAGCACGGTGCTAIGGAT 480 | 481 AIGGIAGGCCAAGAIGCGGIGATCCGCTACTCTCCAAGGCGTGCCGTAACGACCCAIIC 540 | 541 ACCGAAGAGAAATGACGCCATGAACCTCGATGCAAGACGATAGTTCCTTACCTTGAA 600 | 601 AACTAIACGATTGGCCCCGAGGTAGATCATCACAATTGTCAAAGCTGATGTAGCTGGTGGT 660 601 AACTAIACGATTGGCCCCGAGGTAGATCATCAGATTGTCAAAGCTGATGTAGCTGGTGGT 660 | 661 GACGCTGTTCTCACGCCGGTCAGTGCAAGCTGGGCGTTCTTCACATTCAGCCCCAAGGCC 720 | 721 ATGTCAGAGCTCAAGGATGCTGCTACCAAGACTCTTGACGCATCAACAAAGTTCGTGTCG 780 721 ATGTCAGAGCTCAAGGATGCTGCTACCAAGACTCTTGACGCATCAACAAAGTTCGTGTCG 780 | 781 ACTGACGATGCTCTTTCGGCGTTCATCTGGAAATCGGCCTCTCGCGTGCGT | 841 ATCGATGGCTCTGCACCTACCGAGTTCTGCCGTGCTGTTGATGCTCGACCGGCAATGGGT 900 | , 901 GTCTCGAACAACTACCCAGGCCTTCTTCAAAACATGACCTACCACAACTCGACCATCGGC 960 901 GTCTCGAACAACTACCCAGGCCTTCTTCAAAACATGACCTACCACAACTCGACCATCGGC 960 |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yoneyama, K. and Yamaguchi, I.
Trichothecene 3-0-acetyltransferase protects both the producing organism and transformed yeast from related mycotoxins. Cloning characterization of Trill1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (04-FEB-1997) Makoto Kimura, The Institute of Physical and Chemical Research (RIKEN), Microbial Toxicology Laboratory; Hirosawa 2-1, Wako, Saitama 351-01, Japan (E-mail:mkimura@postman.riken.go.jp, Tel:81-048-467-9518,
     GGGCTCGGACTGGGTAAGCCCGAGACTGTG
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                                                                                                                                                                      Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
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| Best Local Similarity 99.3%; Pred. No. 0; Matches 1346; Conservative 0; Mismatches 10; Indels 0; Gaps 0; Dy 1 ATGGCTTTCAAGATACAGCTCGACCCTGGGCGGCTACCAGGCTCCTTTCGATCTAC 60 135 ATGGCTTTCAAGATACAGCTCGACACCCTGGCCAGCTCCTTTCGATCTAC 194 Oy 61 ACCCAAATCAGTCTCTTCTACCCGTTTTCTATTCTCATTTTTTTT | 301 ATGGGAAGGGGGATGCCTATGGGGATGTTTGACG 435 ATGAGAAGGGGGATACCCTATGGGGATGTTTGACG 361 ACGTTACCTATTGGACCTGGTACTGGTCCGACGACG 495 ACGTTACCTATTGGACCTGGTACTGGTCCGACGACGACGACGACGACGACGACGACGACGACGACGA | | 941 ATCGATGGCTCTGCAGGTTCTGGGGGGGGGGGGGGGGGG |

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Gibberella zeae genes for trichothecene 3-O-acetyltransferase, UTP-ammonia ligase and phosphate permease, complete cds.
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/protein_id="BaA29037.1"
/db_xref="GI:2352783"
/translation="WaFKIQLDTLGQLPGLLSIYTQISLLYPVSDPSQYPTIVSTFEQ
GLKRESADVWAVGQVKAEGISBONTGTSPRIPPEDDYRVWYWDLDDPSAPTIEGMR
KAGYPMAMTDENI TAPRATLEIGPGTGPDDPKPVILLQLNFIKGGLILTVNGQHGAMD
WVGQDAVIRLISKACRNDPFTEEBMTAMNLDRKTIVPPTLLQLNFIKGSRY
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/db_xref="taxon:5
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/brotein_id="124290"
/translef="id="34290"
/translef="ton="MarkIQLDTLGQLPGLISIYTQISLLYPVSDPSQYPTIVSTFEQ
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MYGQDAVIRLLSKACRNDPFTEBEMTAMNLDRKTIVPYLENYTIGPEVDHQIVKPDYA
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IMGVGIGGDYPLSSIITSEFATTKWRCAMMAAVFAMQGIGQLVAALVMMFLTLGFKSS
LEQAADTKSCTGDCQIAVDKMWRTLVGFGAVPACIALYYRLTIPETPRYTFDVARDVE
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HVLEIYALFWILGIFTTLLIPETARKTLEELSGEDDYANHDHALESETQASHDKARRT
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| 4716 | 1261 GGCAGTTCTGTGCGGCGCTTTCTCTGAGGATGAG 4776 GGCAGTTCTGTGCGGCGCTTTCTCTGAGGATGAG | CY 1321 ANGARCICAACTAIGGGCAGTACGTTAG 1356 DD 4836 AAGGAGTGGACCAAGTATGCGTTAGGTTAG 4871 | RESULT 6 AP712605 LOCUS AF212605 DEFINITION Gibberella zeae strain NRRL28063 trichothecene | ransferase, partial cd GI:12003706 | ~ | ., Tacke, B.K. and Ca lobal phylogeographi ong lineages of Fusa | fungus causing wheat scab Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7905-7910 (2000) 20346085 10869425 | REFERENCE 2 (bases 1 to 1336) AUTHORS O'Donnell,K. TITLE Direct Submission JOURNAL Submitted (08-DEC-1999) Microbial Promerties Passarch | NCAUR-ARS-USDA, 1815 N. University St., Peoria, IL 61604, USA Location/Qualifiers Source 11336 / Organism="Gibberella zeas" | /mol_type="genomic_DNA" /strain="NRRL28063" /db_xref="taxon:5518" <3>1336 | /product="trichothecene 3-0-acetyltransferase" 3. 11336 | /protein_id="AAG43712.1" /db_xref="G1:120370?" /translation="MAFKIQLDTLGQLPGLLSIYTQISLLYPVSDSSQYPTIVSTFBQ GLKRFSEAVPWVAGGVKARSISEANFGTSFIVPFFTYDPFTYDPFTTPDDGAPTTPCMP | KAGYPWAMFDENIIAPRKTLPIGPGTGPDDPKPVIILQLNFIKGGLILTTNGGGAMD MVGQDAVIRLISKACKNDPFTEESWTAMNLDRKTIVPYLBNYTGPBVDHQIVKADVA GGDAVLTPVSASWAPFTFSPKAMSELKODATKTLDASTKFVSTDDALSAFIWKSADRV RLERLDGSAPPEFCRAVDAFFRAMSELLOMYTHNSTIGRIANSGFGATASRF, | RSELDPASMRQRTRGLATYLHNNPDKSNVSLTADADPSTSVALSSWAKVGLMDYDFGL GLGKCBTVRRPIFBPYBSLMYFMPRKFDGEFCAALSLRDEDMDRLKADKEWT" 317 a 382 c 341 g 296 t ORIGIN | Query Match 98.4%; Score 1334; DB 8; Length 1336; Best Local Similarity 100.0%; Pred. No. 0; Matches 1334; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | CCAGGCCTCCTTTCGATCTAC 60 | CAGC CAGC | |

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| | Oy 181 AAAGCCGAGGGATTAGCGAGGAAACACAGGAACTTCCTTTATCGTCCCTTTTTGAGGAC 2 | 241 GITCCICGEGIGAAGACCTCCGCGAIGATCCTCACGCCCACGAIGAGGGGT 3 | QY 301 Db 303 | Qy 361 ACGTTACCTATTGGACCTGGTACTGGTCCCGACGACCCAAAGCCTGTAATTCTATTGCAG 420 | Oy 421 CTCAACTTCATCAAGGGGGACTCATCCTCACTGTCAAGGGACAGGACGGTGCTATGGAT 480 | Oy 481 AIGGTAGGCCAAGAIGCGGTGAICCGICTACTCTCCAAGGCGTGCCGTAACGAITC 540 | OY 541 ACCGAAGGAAATGACGGCCATGAACCTCGATCGCAAGACGATAGTTCCTTAGAA 600 | Oy 601 AACTATACGATGGCCCCGAGGTAGATCATCAGATTGTCAAAGCTGATGTAGCTGGTGGT 660 | Qy 661 GACGCTGTTCTCACGCCGGTCAGTGCAAGCTGGGCGTTCTTCACCTTCAGCCCCAAGGCC 720 | OY 721 ATGTCAGAGCTCAAGGATGCTGCTACCAAGACTCTTGACGCATCAAAGTTCGTGTCG 780 | QY 781 ACTGACGATGCTCTTTCGGCGTTTCATCTGGAAATCGGCCTCTCGCGTGCGT | QY 841 ATCGATGGTCTGGACCTACCGAGTTCTGCCGTGCTGTTGATGCTCGACTGGCT 900 DD 843 ATCGATGGCTCTGCACCTACCGAGTTCTGCCGTGCTGTTGATGCTCGACTGGCAATGGGT 900 | MND 901 GTCTCGAACAACTACCCAGGCCTTCTTCAAAACATGACCTACCACAACTCGACCATCGGC 960 | OY 961 GABATCGCCAACGAGTCACTCGGCGCAACAGCATCACGCCTTCGTTCAGAACTCGACCCC 1020 | QY | OY 1081 TCCAACGTATCCCTGACGCTGATGCGGACCCATCTACCAGCGTCATGCTGGGTTCTTGG 1140 | QY 1141 GCCAAGGTGGGACTCTGGGATTACGACTTGGGCTCGGACTGGGTAAGCCCGAGACTGTG 1200 0 1143 GCCAAGGTGGGACTCTGGGATTACGACTTTGGGCTCGGACTGGGTAAGCCCGAGACTGTG 1202 | |
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| 1203 AGACGGCCAATCTTTGAGCCTGTTGAGAGCTTGATGTACTTTATGCCCAAGAAGCCTGAT 12 | 1261 | Oy 1321 AAGAGTGGACCAA 1334 | RESULT 8 AF212603 LOCUS AF212603 DRF linear PLN 26-JUN-2001 | ACCESSION AF712603.1. GI:12003702 KRYWORDS | SOURCE Gibberella zeae ORGANISM Gibberella zeae Entaryota; Rungi, Ascomycota; Pezizomycotina; Sordariomycetes; Hynorpemyreridae, Hynorpeales, Norteinas, Sordariomycetes; | Gibberella. asper, H.H. ic structure | מד מווו' | | NCAUR-ARS | /organisml= cropsferia zeae /mol type="genomic DNA" /strain="NRRL6394" /db xref="taxon:5518" /3 _ >1336 | | SS | KAGY PANANDEN II THARKTIP IGREGARIA SIET I VERDIVER VA KULKUDENAFILLEGIRK KAGY PANANDEN II TAPRKTIP IGREGAPOTGPIDEKPYLLIGUINFIKGELILIYNIGGIGAMD WYGQDAYTRIJSKACRNDPFTEEMTAANNIDRKTIVPYLLENYTIGPEVDHQIVKPDVA GGBAVLTPYRAFFIRESPRANGELGOATKILGASTKEVSTDDALASHINKEGARV RIERI IDGSAPTEFCRAVIDR PANANSKINVPGTI IONAMYHNIGHTGETANGSTAANA GET | RSELDPASNEQETICATYLHUNDPKSINZALTADADPSTSVALIZADADPSTSVALI | / Match Local Similarity 99.9%; Pred. No. 0; les 1332; Conservative 0: Mismatches 2: Indels 0: Gane | 1 ATGGCTTTCAAGATACAGCTCGACACCTCGGCCAGCTACCAGGCCTCCTTTCGATCTAC 60 | 61 ACCAAATCAGTCTCCTCTACCCGTCTCTGATTCCTCTCAATATCCCACTATTGTCAGC 12 | |

| | 301 ATGAGAAAGGGGGATACCCTATGGCGATGTTTGACGAGAACATCATCGGGCCAAGGAAG 360 303 ATGAGAAAGGCGGGATACCCTATGGCGATGTTTGACGAGAACATCATCGCGCCAAGGAAG 362 361 ACGATACCTATTGGACCTGGTCCCGACGACGACGACGTAATTCTATTGCAG 420 361 ACGTTACCTATTGGACCTGGTCCCGACGACGACGAAAGCCTGTAATTCTATTGCAG 420 363 ACGTTACCTATTGGACCTGGTACTGGTCCCGACGACGACCTGTAATTCTATTGCAG 420 | 421 CTCAACTTCATCAAGGGGGACTCATCCTCACTGTCAACGGACAGGTGCTATGGAT 480 423 CTCAACTTCATCAAGGGGGGACTCATCCTCACTGTCAACGGACAGGCGCTGTTGTTTTTTTT | | | 903 GTCTCGAACAACTACCCAGGCCTTCTTCAAAAATGTGACCTACCACAACTCCACCACAACTCGACCAACTCGACCAACTCCACCAACTCGACCAACTCCACCAACTCGACCAACTCGACCACCAACTCGACCCCC 1020 961 GAAATCGCCAACGAGTCACTCGGCGAACAGCATCACGCCTTCGTTCAGAACTCGACCCC 1020 1021 GCGAGCATGCGCAACAAGAACACACAACACCACACACCCCGACAAG 1080 1023 GCGAGCATGCGCAACAAGAAGAGTCTCGCAACGTACCTGCACAACACCCCGACAAG 1080 1081 TCCAACGTATCCCTGACACAAGAGGTCTCGCACGTACCTGCACAACACCCCGACAAG 1080 1082 TCCAACGTATCCCTGACCGCTCATGCGCACGTACCTGCACAACATCTTGG 1140 11083 TCCAACGTATCCTGGCATTACGACTTTGGGCTCACCGCACAGACTCTTGG 1140 1141 GCCAAGGTGGGACTCTGGGGACTTTGGGCTCGGACTCGGACTGGTAAGCCCGAGACTGTG 1200 1143 GCCAAGGTGGGACTTTGGAGCTTTGGGCTCGGACTGGGTAAGCCCGAGACTGTG 1200 1141 GCCAAGGTGGGACTTTGGAGCTTTTTAGGCTCGGACTGGTTAAGCCCGAGACTGTG 1200 11201 AGACGGCCAATCTTTGAGCCTTTTAGGCTCGGACTGGTTAAGCCCCGAGACTGTGT 1260 1201 AGACGGCCAATCTTTGAGCCTTTTAAGGCTCGAACAAGCCTGAT 1260 1201 AGACGGCCAATCTTTTAAGACTTTAATGCCCCAAGAAGCCTGAT 1260 |
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| Db 1203 AGACGGCCAATCTTTGAGCCTGTTGAGGGTTGATGTACTTTATGCCCCAAGAAGCCTGAT 1262 Qy 1261 GGCCAGTTCTGTGCGGCGCTTTCTCTGAGGATGAGGACGACTGATGAAGGCGGAT 1320 Db 1263 GGCGAGTTCTGTGCGGCGCTTTCTCTGAGGATGAGGATATGGACCGATTGAAGGCGGAT 1322 Qy 1321 AAGGAGTGCACAA 1334 Db 1323 AAGGAGTGGACCAA 1336 | RESULT 9 AF212606 LOCUS AF212606 LOCUS AF212606 AF212606 DEFINITION Gibberella zeae strain NRRL28336 trichothecene 3-0-acetyltransferase, partial cds. ACCESSION AF212606 VERSION AF212606.1 GI:12003708 | KEYWORDS KEYWORDS Gibberella zeae ORGANISM Gibberella zeae Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella. REFERENCE 1 (bases 1 to 1336) AUTHORS O-Donnell, K., Kistler, H.C., Tacke, B.K. and Casper, H.H. Gene genealogies reveal global phylogeographic structure and reproductive isolation among lineages of Fusarium graminearum, the fungus causing wheat scab JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7905-7910 (2000) MEDITNR 20145085 | 10869425 2 (bases 1 t 0 Donnell, K. Direct Submis Submitted (08 NCAUR-ARS-USD LOCA | /organism="Garborella Zeae" /organism="Garborella Zeae" /btrain="NRRL28336" /db xref="taxon:5518" /db xref="taxon:5518" /31336 /product="trichothecene 3-0-acetyltransferase" /codon_start=1 /product="trichothecene 3-0-acetyltransferase" /product="trichothece | GGDAVLTPVSASWAFFTFSPKAMSELKDAATKTLDASTKEVSTDDALSAFIWKASRRV REBRIDGASPFERCRAYDARPANGVSNNYPGLLQNMTYTRNSTIGETANBELGATASRL REBRIDGASPFERCRAYDARPANGVSNNYPGLLQNMTYTRNSTIGETANBELGATASRL REBRIDGASWAGARTGAATVLHANPDKSNVSLTADADFSTSVMLSSWAKVGLWADVFGL GLGKPETVRRPIFEPVESLMYFMPKKPDGFFCAALSLRDEDMDRLKADKEWT" ORIGIN Query Match Query Match Sest Local Similarity 99.9%; Pred. No. 0; Matches 1332; Conservative 0; Mismatches 2; Indels 0; Gaps 0; Matches 1332; Conservative 0; Mismatches 2; Indels 0; Gaps 0; Original Argoritrchagaracaccccaccaccaccaccaccaccaccaccaccacca |

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                                   ACCTTCGAGCAAGGTCTTAAGCGCTTCTCCGAAGCCGTCCCATGGGTCGCAGGCCAGGTC 182
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                                                                                                                              AAAGCCGAGGGCATTAGCGAGGAAACACAGGAACTTCCTTTATCGTCCCTTTTGAGGAC
                                                                                                                                                                              GITCCTCGTGTTGTAGTGAAGACCTCCGCGATGATCCTTCAGCGCCCACGATCGAGGGT
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Gibberella zeae
Gibberella zeae
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomyceridae; Hypocreales; Nectriaceae; Gibberella.
1 (bases 1 to 1336)
O'Donnell, K., Kistler, H.C., Tacke, B.K. and Casper, H.H.
Gene genealogies reveal global phylogeographic structure and reproductive isolation among lineages of Fusarium graminearum, fungus causing wheat scab
Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7905-7910 (2000)
20345085
                                                                                     GECGAGTICTETTCTCTCTCTCTCAGGGATGAGGATATGGACCGATTGAAGGCGGAT
                                               GGCGAGTICTGTGCGCGCTTTCTCTGAGGGATGAGGATATGGACCGATTGAAGGCGGAT
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O'Donnell,K.
Direct Submission
Submitted (08-DEC-1999) Microbial Properties Research,
NCAUR-ARS-USDA, 1915 N. University St., Peoria, IL 61604, USA
Location/Qualifiers
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/protein_id="AAG43714.1"
/db_xref="GI:12003711"
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/product="trichothecene 3-0-acetyltransferase"
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/wol_type="genomic DNA"
/strain="NRRL28439"
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| Db 1203 AGACGGCCAATCTTGAGCCTGTTGAGAGCTTGATGTACTTTATGCCCAAGAAGCCTGAT 1262 | PRESEURT 11 ACCESSION ACCESSION |

| | 361 A | 421 CTCAACTTCATCAAGGGCGGACTCATCTCACTGTCAACGGACAGCACGGTGCTATGATT [| QY 541 ACCGAAGGAAATGACGCCATGAACCTCGATCGCAAGACGATAGTTCCTTACCTTGAA 600 Db 543 ACCGAAGAGAAATGACGCCATGAACCTCGATCGCAAGACGATAGTTCCTTACCTTTGAA 602 QY 601 AACTATACGATTGGCCCCGAGGTAGATCATCAGATTGTCAAAGCTGATGTAGCTGGTGGT 600 Db 603 AACTATACGATTGGCCCCGAGGTAGATCATCAGATTGTCAAACCTGATGTAGCTGGTGGT 660 | | QY 781 ACTGACGATGCTCTTTCGGCGTTCATCTGGAAATCGGCCTCTCGCGTGCGT | | QY 1021 GCGAGCATGCGCCAGCGGAACAAGAGGTCTCGCGACGACAACAACAACAACACCCGGACAAG 1080 Db 1023 GCGAGCATGCGCCAGCGAACAAAGAGGTCTCGCGACCTCGCACAACAACAACAAG 1082 QY 1081 TCCAACGTATCCCTGACGTGATGCGGACCCATCTACCAGCGTCATGCTGAGTTCTTGG 1140 Db 1083 TCCAACGTATCCCTGACGGCTGATGCGGACCCATCTACCAGGTCATGCTGAGTTCTTGG 1142 | QY 1141 GCCAAGGTGGGACTCTGGGATTACGACTTTGGGCTCGGACTGGGTAAGCCCGAGACTGGT 1200 Db 1143 GCCAAGGTGGGACTCTGGGACTTTGGGCTCGGACTGGGTAAGCCCGAGACTGTG 1202 Qy 1201 AGACGGCCAATCTTGAGCTTGTTGAGGCTTGATGTATTATGCCCCAAGAAGCCTGAT 1260 |
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| Db . 1203 AGACGGCCAATCTTTGAGCCTGTTGAGGGCTTGATGTACTTTATGCCCAAGAAGCCTGAT 1262 Qy 1261 GGCGAGTTCTGTGCGGCGCTTTCTCTGAGGGATATGGACCGATTGAAGGCGGAT 1320 Db 1263 GGCGAGTTCTGTGCGGCGCTTTCTCTGAGGGATATGGACCGATTGAAGGCGGAT 1322 Qy 1321 AAGCAGTGCACCAA 1334 Db 1323 AAGCAGTGGACCAA 1336 | RESULT 12 AF212604 LOCUS AF212604 LOCUS DEFINITION Gibberella zeae strain NRRL13383 trichothecene ACCESSION AF212604 VERSION AF212604.1 GI:12003704 | KEYWORDS Gibberella zeae SOURCE SOURCE SOURCE SURANISM Gibberella zeae SURANISM Gibberella zeae SURANISM Gibberella zeae Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella. REFERENCE 1 (bases 1 to 1336) AUTHORS O'Donnell,K., Kistler,H.C., Tacke,B.K. and Casper,H.H. TITLE Gene genealogies reveal global phylogeographic structure and reproductive isolation among lineaes of Finarium creminearum the | | PERTURES NCAUR-ARG-USDA, 1815 N. University St., Peoria, IL 61604, USA FEATURES Location/Qualifiers Source /organism="Gibberella zeae" /mol type="genomic DNA" /strain="NRRL13383" /db xref="taxon:5518" | | GALKAE BAAVEWARGOVALEL BEGNITGTSF TYPEEDYBRVOVEDIBDDEARPTIEGHR KAGTEMAMPDENIIA PREKTILP 1GPGTGPDDPRPVILLIQUINFIKGGLILTVNGGJGAMD MVGQDAVIRILISKACRNDPFTEEEMTAMNILDRYTILLQLINFIKGGLILTVNGGJGAMD MVGQDAVIRILISKACRNDPFTEEEMTAMNILDRYTILQUINFIKGGLILTVNGGJGAN GGDAVITLDVGSAMPFTEFSKAMSEIKDAATKYTILDASTKEVSTDDALSAFTWKSARV RLERIDGSAPTEFCRAVDARPAMGVSNNYPGLILQUNTNSTIGETANESIGATASRI. RSELDPASMORTRGIATTYLHNNPDRSSNVSILTADADPSTSVNLSSNAKVGIMDYDFGI. GLGRPETVRRPIFEFVESIMYFMFKKPDGEFCAALSIRDEDMDRIKADKEWT" ORIGIN | <pre>y Match Local Similarity 99.8%; Pred. No. 0; hes 1331; Conservative 0; Mismatches 3; Indels 0; Gaps 1 ATGGCTTTCAAGATACAGCTCGACACCTCGGCCAGCTACCAGGCTCCATTCCATCTACAGTACAGTACAGCTAGAGATACAGCTAGACAGCTAGAGATACAGCTAGAGATACAGCTAGAGATACAGCTAGAGATACAGATACAGATACAGATACAGATACAGATACAGATACAGATACAGATACAGATACAGATACAGATACAGATACAGATAGAT</pre> | 6 6 12 12 |

| | | 421 CTCAACTTCATCAAGGGGGACTCATCCTCAACGGACAGCACGGTGCTATGGAT 480 423 CTCAACTTCATCAAGGGGGGGACTCCTCATTCTCAACGGACACACGGTGCTATGGAT 482 481 ATGGTAGGCCAAGATGCGGTGATCCGTCTACTTCCAAGGCCTGCCGTACCTTC 540 483 ATGGTAGGCCAAGATGCGGTGATCCGTCTACTTCCAAGGCGTGCCGTACCATTC 540 484 ATGGTAGGCCAAGATGCGGTGATCGTCTACTTCCAAGGCGTGCCGTACCATTC 540 545 ACCGAAGAGGAAATGACGCTCTACTCGATGCCAAGACGTCCTTGAA 600 546 ACCGAAGAGGAAATGACGCATGAACCTCGATGCCAAAGACGATAGTTCCTTGACTTGAA 602 547 ACCGAAGAGGAAATGACGCCATGAACCTCGATGGCAAGACGATAGTTCCTTGAA 602 | a AACTATACGATTGGCCCCGAGGTAGATCATCAGATTGTCAAAGCTGATGTGGCTGGTGGTGGT b AACTACACGATTGGCCCCGAGGTAGATCATCAGATTGTCAAACCTGATGTAGCTGGTGGT cacgattgtctcacgattgtcacattgtcacattcaca | 723 ATGTCAGAGCTCAAGGATGCTACCAAGACTGTTGACGCATCAACAAAGTTCGTGTCG 782 781 ACTGACGATGCTCTTTCGGCGTTCATCTGGAAATCGGCCTCTCGCGTGCGT | GCGAGCATGAGTCACTCGGCGCACCACATCA GCGAGCATGCGCCAGCGACAGCATCA GCGAGCATGCGCCAGCGACAGGTCTCGCGACG GCGAGCATGCGCGCACCACCACCACCACCACCACCT TCCAACGTTCCTGACGCTGACGACCACCT TCCAACGTTCCTGACGATTACGACACCCATCT GCCAAGGTGGGACTCTGGGATTACGACTTTGGGTTC GCCAAGGTGGGACTCTGGGATTACGACTTTGGGTTC AGACGGCCAATCTTGAGATTACGACTTTGGGTTC AGACGGCCCAATCTTGAGACTTTGGGTTC AGACGGCCCAATCTTGAGACTTTGGGTTC |
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1203 AGACGGCCAATCTTTGAGCCTGTTGAGAGCTTGATGTACTTTATGCCCAAGAAGCCTGAT 1262 Search completed: February 7, 2004, 20:53:19 Job time : 5224 secs 1321 AAGGAGTGGACCAA 1334 |||||||||||||| 1323 AAGGAGTGGACCAA 1336 S d Dp à

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OM protein - protein search, using sw model

February 7, 2004, 21:53:49; Search time 553 Seconds (without alignments) 129.450 Million cell updates/sec Run on:

US-10-614-954-6 Title:

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1107863 seqs, 158726573 residues Searched:

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1107863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Description | Trichothecene resi F. graminearum tri Trichothecene resi Sequence encoding Arabidopsis thalla | Arabidopsis thalia Wheat stress respo Arabidopsis thalia Arabidopsis thalia |
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| QI | AAB03935 AAY51848 AAB03934 AAB03936 AAG18711 | AAG18710 ABU58179 AAG18709 AAG48446 |
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| | Herbicidally activ | | | Sovbean stress res | dally a | _ | dopsis th | ξĎ | Aromatic acyl tran | allý a | | Herbicidally activ | 'n | Arabidopsis thalia | H | Arabidopsis thalia | rΉ | Arabidopsis thalia | Arabidopsis thalia | 1, | Arabidopsis thalia | Arabidopsis thalia | Taxus cuspidata fu | Herbicidally activ | Arabidopsis thalia | Arabidopsis thalia | Herbicidally activ | Arabidopsis thalia | Polypeptide encode | Tobacco Ant32 geno | Arabidopsis thalia | ω | Ø | 7 | Taxus cuspidata fu |
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| AAG48445 | ABB93749 | AAG48444 | ABU58173 | ABU58177 | ABB93641 | AAB36457 | AAG24209 | AAG24208 | AAW04724 | ABB92609 | ABB92606 | ABB92608 | ABB92607 | AAG46685 | ABB93668 | AAG46684 | ABB93310 | AAG37720 | AAG37735 | ABB93930 | AAG37734 | AAG37719 | AAE00254 | ABB91119 | AAG46686 | AAG21060 | ABB93980 | AAG21059 | AAR47475 | AAR46929 | AAG25750 | AAG45712 | AAG45711 | ABB93588 | AAE00240 |
| 21 | 23 | 21 | 24 | 24 | 23 | 21 | 21 | 21 | 17 | 23 | 23 | 23 | 23 | 21 | 23 | 21 | 23 | 21 | 21 | 23 | 21 | 21 | 22 | 23 | 21 | 21 | 23 | 21 | 15 | 15 | 21 | 21 | 21 | 23 | 22 |
| 433 | 433 | 449 | 446 | 439 | 442 | 431 | 428 | 440 | 448 | 459 | 450 | 648 | 443 | 441 | 441 | 457 | 475 | 426 | 426 | 426 | 438 | 442 | 448 | 436 | 327 | 448 | 448 | 455 | 448 | 448 | 313 | 479 | 484 | 484 | 439 |
| 7.3 | 7.3 | 7.3 | 7.2 | • | 6.7 | • | 9.9 | ٠ | 6.5 | | 6.4 | 6.4 | • | • | • | | 6.1 | • | • | 6.1 | • | • | • | • | • | • | ٠ | | • | • | • | • | 5.7 | | |
| | Ψ. | ď | 168.5 | 9 | • | 54. | 154 | L) | 51. | | 149.5 | 4 | 4 | 4 | 4 | 4 | 4 | | | ď | | $^{\circ}$ | 142 | 41 | 38 | 34 | 134.5 | 134.5 | 134 | 134 | 32 | 32 | 132.5 | 132.5 | 132 |
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| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

ALIGNMENTS

AAB03935 standard; Protein; 451 AA. (first entry) 26-FEB-2001 AAB03935; RESULT 1 AAB03935

Tricothecene resistance, resistant; crop protection; mycotoxin; fungus; wheat; maize; barley; rice; heterologous gene; transformation; Fusarium. Trichothecene resistance polypeptide.

Pusarium graminearum

WO200060061-A2.

12-OCT-2000.

29-MAR-2000; 2000WO-EP02769.

31-MAR-1999; 99US-0282995. 11-FEB-2000; 2000US-0502852.

(NOVS) NOVARTIS AG. (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.

Dawson JL; Salmeron JM, Reed JN, Hohn TM, Peters C,

WPI; 2000-679374/66. N-PSDB; AAA54209.

activity

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This invention describes a novel protein with trichothecin 3-0-acetyltransferase activity. The gene is used as a selective marker in a gene manipulation using eukaryote as the host cell. This sequence represents the trichothecin 3-0-acetyltransferase isolated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 MSELKDAATKTLDASTKFVSTDDALSAFIWKSASRVRLERIDGSAPTEFCRAVDARPAMG
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                                                                                                                                                                                                                                    Trichothecin 3-O-acetyltransferase gene useful as a selective marker gene manipulations in eukaryotic host cells -
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0; Mismatches 4,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TLPIGPGTGPDDPKPVILLQLNFIKGGLILTVNGQHGAMDMVGQDAVIRLLSKACRNDPF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TEEEMTAMNLDRYTIVPYLENYTIGPEVDHQIVKADVAGGDAVLTPVSASWAFFTFSPKA
                                                                                                                                                           A heterologous gene encoding a gene product which confers trichothecene resistance can be used to transform plant cells to make them resistant to fungal infection. The transformation method is useful for preventing mycotoxin contamination of a plant, particularly a crop plant such as wheat, maize, barley or rice, and for reducing and/or preventing the growth of a fungus of the genus Fusarium that produces a trichothecene, preferably comprising a C-3 hydroxyl group, by growing transformed crop plants in an area which is moderate to severe fungal infestation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MSELKDAATKTLDASTKFVSTDDALSAFIWKSASRVRLERIDGSAPTEFCRAVDARPAMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 MSELKDAATKTLDASTKFVSTDDALSAFIWKSASRVRLERIDGSAPTEFCRAVDARPAMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VSNNYPGLLQNMTYHNSTIGEIANESLGATASRLRSELDPASMRQRTRGLATYLHNNPDK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 VSNNYPGLLQNMTYHNSTIGEIANESLGATASRLRSELDPASMRQRTRGLATYLHNNPDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MAFKIQLDTLGQLPGLLSIYTQISLLYPVSDSSQYPTIVSTFEQGLKRFSEAVPWVAGQV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MARKIQLDTLGQLPGLLSIYTQISLLYPVSDSSQYPTIVSTFEQGLKRFSEAVPWVAGQV
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                    Plant cell for preventing mycotoxin contamination of wheat, maize, barley or rice plant, comprises heterologous polynucleotide encoding gene product expressed in cell, having trichothecene resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                               ·;
                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 2334; DB 21; Length 451; 100.0%; Pred. No. 5.4e-211; tive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     graminearum trichothecene 3-0-acetyltransferase protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Trichothecene 3-0-acetyltransferase; selective marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          451
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                                                                                                                           Page 49-50; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard; Protein; 451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 451; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fusarium graminearum.
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                                                                                                                                                                                                                                                                                                                                                                    451 AA;
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                                                                                                                           Claim 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           A heterologous gene encoding a gene product which confers trichotheceme resistance can be used to transform plant cells to make them resistant to fungal infection. The transformation method is useful for preventing mycotoxin contamination of a plant, particularly a crop plant such as wheat, maize, barley or rice, and for reducing and/or preventing the growth of a fungus of the genus Fusarium that produces a trichotheceme, preferably comprising a C-3 hydroxyl group, by growing transformed crop plants in an area which is moderate to severe fungal infestation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 AEGISEGNTGTSFIVPFEDVPRVVVKDLRDDPSAPTIEGMRKAGYPMAMFDENIIAPRKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71 TEGISEGNIGISKIIPYEETPRLVVKDIRDDSSAPTIEGLRKAGFPLEMFDENVVAPRKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LPIGPGTGPDDPKPVILLQLNFIKGGLILTVNGQHGAMDMVGQDAVIRLLSKACRNDPFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 AFKIQLDTLGQLPGLLSIYTQISLLYPVSDSSQYPTIVSTFEQGLKRFSEAVPWVAGQVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            310 SSTYPGLLONMTYHDSTVAEIANEPLGATASRLRSELNSDRLRRRTQALATYMHGLPDKS
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                                                                                                                                                                                                                                                                                                                                                 Plant cell for preventing mycotoxin contamination of wheat, mai:
barley or rice plant, comprises heterologous polynucleotide enco
gene product expressed in cell, having trichothecene resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 21; Length 459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79.7%; Score 1860.5; DB 21; Lengt 77.6%; Pred. No. 2.4e-166; ive 50; Mismatches 50; Indels
                                                                                                                                                                                                                                                                     Dawson JL;
fungus; wheat; maize; barley; rice; heterologous gene;
                                                                                                                                                                                                                                                                     Reed JN,
                                                                                                                                                                                                                    (NOVS ) NOVARTIS AG.
(NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 15; Page 46-48; 62pp; English.
                                                                                                                                                                                                                                                                     Salmeron JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77.6%;
                                                                                                                                           29-MAR-2000; 2000WO-EP02769.
                                                                                                                                                                       31-MAR-1999; 99US-0282995.
11-FEB-2000; 2000US-0502852.
                                              Fusarium sporotrichioides
              transformation; Fusarium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                     Hohn IM, Peters C,
                                                                                                                                                                                                                                                                                                     WPI; 2000-679374/66
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            459 AA;
                                                                                                                                                                                                                                                                                                                  N-PSDB; AAA54206
                                                                                                           12-OCT-2000
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82 DEGNTGTYRIVPSDKIP-LIVQDLREDLSAPTMDSLEKADFPIYMLDEKTFAPCMTINPP 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125 GPGTG-PDDPKPVILLQLNFIKGGLILTVNGQHGAMDMVGQDAVIRLLSKACRNDPFTEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plant cell for preventing mycotoxin contamination of wheat, maize, barley or rice plant, comprises heterologous polynucleotide encoding gene product expressed in cell, having trichothecene resistance
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tricothecene resistance; resistant; crop protection; mycotoxin; fungus; wheat; maize; barley; rice; heterologous gene; rransformation; Fusarium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dawson JL;
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence encoding trichothecene resistance polypeptide
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44.4%; Pred. No. 1.2e-81;
ive 84; Mismatches 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Reed JN,
451
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(NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MEH.
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                              422 EFCAALSLRDEDMDRLKADKEWTKYAQYVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 15; Page 51-52; 62pp; English.
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                                                                                                                                                                                                                            AAB03936 standard; Protein; 474
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11-FEB-2000; 2000US-0502852.
                                                                                                                                                                                                                                                                                                                                                             entry)
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202; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                          (first
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      24-MAY-1999;
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27-MAY-1999;
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02-AUG-1999;
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260 ISLQNLRILAMQTCTSGTKFVSTDDIVTARIWKSVSRARLSRLKPETKSNLGRAVDVRKR 319
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                                                                                                       CPDXTKVSIPQPIDTLSGIMVSSWAKVSLYDVDFNLGLGKPKSVRRPRFISLESLIYFMP 439
EMTAMNLDRKTIVPYLENYTIGPEVD--HQIVKA--DVAGGDAVLTPVS-ASWAFFTFSP 238
         KAMSELKDAATKTLDASTKFVSTDDALSAFIWKSASRVRLERIDGSAPTEFCRAVDARPA 298
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                                                                                                                                                                                                                                                   Protein identification, signal transduction pathway, metabolic pathway, hybridisation assay, genetic mapping, gene expression control, promoter, termination sequence.
                                                                                               NPDKSNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGLGKPETVRRPIFEPVESLMYFMP
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                                                                                                                                        KKPDGEFCAALSLRDEDMDRLKADKEWTKYAQYVG 451
                                                                                                                                                                                    AAG18711 standard; Protein; 424 AA
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                                                                                                                                                                                142 NFIK-GGLILITVNGQHGAMDMVGQDAVIRLLSKACRNDPFTEEEMTAMNLDRKTIVPYLE 200
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                                                                                                                36 PIIVSTF--EQGLKR-FSEA-VPW--VAGQVKAEG----ISEGNIGISFIVPFEDVPRV
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                                                                                                                                                                                                                                                                  Length 433;
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                                                                                                                                                                                                                                                               DB 21;
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Pred. No. 4.8e-07;
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response proceins (including peptide-methionine sulphoxide reductases) appearing as ABUS8148-ABUS8246 (or a protein 80% identical to them) from Zea mays, Oryza sativa, Glycine max, or Triticum aestivum. Also included are expression cassettes, transformed host cells, transformed proteins of a particular and a computer system/data processing system for identifying, analysing, or modelling a genetic sequence. The plant nucleic acid is useful in developing strategies to improve plant response to stress (e.g. drought, heat, radiation or pathogen attack), engineering plants with increased disease and stress resistance, manipulating DNA repair and recombination efficiency,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    improving plant response to stress, engineering plants with increased disease and stress resistance, or and improving/protecting grain flavor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New peptide-methionine sulfoxide reductase and nucleic acids, useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    manipulating intracellular protein transport, and improving/protecting grain flavour. The nucleic acids may also be used as probes or amplification primers in the detection, quantitation or isolation of ge transcripts, for recombinant expression of encoded polypeptides, as immunogens in preparing or screening antibodies, and in sense or antisense suppression of one or more genes in a host cell, tissue or plant. The proteins may be used as immunogens or antigens to obtain antibodies specifically immunoreactive with the protein, and in assays for enzyme agonists or antagens: the present sequence is a plant stress response protein (or fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to isolated nucleic acids encoding plant stress
             heat; radiation; pathogen attack; grain flavour; disease resistance; peptide-methionine sulphoxide reductase; DNA repair; enzyme; intracellular protein transport.
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Plant; EST; expressed sequence tag; stress response; drought;
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Weng Z;
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99US-137667P.
2000US-0566394.
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99US-133436P.
99US-133437P.
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ODELL J T.
RAFALSKI J A.
THORPE C J.
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WENG Z.
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Thorpe CJ,
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(THOR/)
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(WENG/)
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(ODEL/)
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Score 170.5; DB 24; Length 436;

Pred. No. 4.9e-07;

7.3%;

Query Match Best Local Similarity

436 AA;

Sequence

ABU58179 standard; Protein; 436 AA

Wheat stress response protein #7.

(first entry)

14-APR-2003

ABU58179

ABU58179
ID ABU5
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AC ABU5
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DT 14-A
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990S-0139461
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15;
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                                                                                                                                         | :: | | :: | | :: | G----APRPFVTRVYSVSQKLLADIKSRCAPG-----VSTYGAVTAHLWRCMCVARGL 273
                                                                                                                                                                            274 APGSDTRLRVPANIRHRLRPQLPRQFFGNAIVRDLVTVK--------VGDVL 317
                                                                                                                                                                                                     NESLGATASRIRSELDPASMRORTRGLATYLHNNPDKSNVSLTADADPSTSVMLSSWAKV 383
                                                                                                                                                                                                                       SOPLGYVADTIRKAVDHVD-DAYTRSVIDYLEVESEKGSOAARGOLMPESDLWVVSWLGM 376
                  56 VAGQVKAEGISEGN----TGTSFIVPFEDVPRVVVKDLRDDPSAPTIEGMRKAGYPMA 109
                                                      110 MFDENIIAPRKTLPIGPGTGPDDPKPVILLQLNFIK-GGLILTVNGQHGAMDMVGQDAVI 168
                                                                                         --LSKACRNDPFTEEEMTAMNLDRKTIVPYLENYTIGPEVDHQIVKADVAG 219
                                                                                                          QTWTGLARGLSLSEACPSPPHDRTLLRARSPPR-------PEFEHPVYSPAYLN 224
                                                                                                                                                                  ---SASRVRL----ERIDGSAPTEFCRAVDARPAMGVSNNYPGLLONMTYHNSTIGELA 323
                                                                                                                                                                                                                                                                                                                                                                               Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                             ----PSG-----DPPCHMAMFQVTFLKCGGVVLGTGIHHVTMDGMGAFHFI
                                                                                                                             GDAVLTPVSASWAFFTFSPKAMSELKDAATKTLDASTKFVSTDDALSAFIWK-----
61; Mismatches 158; Indels 109; Gaps
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99US-0132048.
99US-0132407.
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64-MAY-1999;
05-MAY-1999;
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25-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              298 AMGVSNNYPGLLQNMTYHNSTI-----GEIANESLGATASRLRSELDPAS 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   343 MRQRIRGLATYLHNNPDKSNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKPETVRR 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         142 NFIK-GGLILTVNGQHGAMDMVGQDAVIRLLSKACRNDPFTEEEMTAMNLDRKTIVPYLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  253 VALK--AKSKEDGNTVSYSSYEMLAGHVWRSVGKAR--GLPNDQETKLYIATDGRSRLRP
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                                                                                                                                                                                                                                                                                                                                   tch 7.3%; Score 170.5; DB 21; Length 450; al Similarity 23.4%; Pred. No. 5.1e-07; 107; Conservative 61; Mismatches 153; Indels 137;
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99US-0160815.
99US-0160980.
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99US-0161404.
99US-0161405.
99US-0161360.
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99US-0161992.
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22-0CT-1999;
22-0CT-1999;
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25-0CT-1999;
26-0CT-1999;
26-0CT-1999;
26-0CT-1999;
28-0CT-1999;
28-0CT-1999;
28-0CT-1999;
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12-JUL-1999; 13-JUL-1999; 14-JUL-1999; 15-JUL-1999; 16-JUL-1999; 19-JUL-1999; 19-JUL-1999; 19-JUL-1999; 19-JUL-1999; 19-JUL-1999; 19-JUL-1999; 19-JUL-1999; 19-JUL-1999; 20-JUL-1999;

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RR 12-MR.1999; 9910-112182.
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RR 12-MR.1999; 9910-112182.
RR 12-MR.1999; 9910-112183.
RR 11-MR.1999; 9910-112183.
RR
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06-AUG-1999

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L6-AUG-1999

23-AUG-1999;

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02-AUG-1999; 02-AUG-1999; 02-AUG-1999;

04-AUG-1999; 04-AUG-1999;

05-AUG-1999 05-AUG-1999 06-AUG-1999

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Arabidopsis thaliana
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08-APR-1999;
16-APR-1999;
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14-MAY-1999;
14-MAY-1999;
14-MAY-1999;
14-MAY-1999;
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29-MAR-1999;
01-APR-1999;
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20-MAY-1999;
21-MAY-1999;
24-MAY-1999;
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09-MAR-1999;
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21-APR-1999;
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23-APR-1999;
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28-MAY-1999
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                                                               AAG48445;
    RESULT 10
                     AAG48445
                                   HERE IN THE SET IN THE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               299 MGVSNNYPGLLQNMTYHNSTI-------GBIANESLGATASRLRSELDPASM 343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----YLEMQPDLSALVRGAHTYKCPNLGITSWVRLPIYDADFGWG------RP
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29-OCT-1999;
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                        Arabidopsis thaliana protein fragment SEQ ID NO: 61176.
AAG48445 standard; Protein; 433 AA.
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99US-0130449.
99US-0130510.
99US-0130891.
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                                                          (first entry)
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| UIS - 0139459 UIS - 01394610 UIS - 01394610 UIS - 0139463 UIS - 0139750 UIS - 0139750 UIS - 0140353 UIS - 01406955 UIS - 01406955 | 99US-0141842. 99US-0142154. 99US-0142390. 99US-0142390. 99US-0142390. 99US-0142970. 99US-0142977. 99US-0143624. 99US-0144085. 99US-0144085. 99US-0144331. 99US-0144331. 99US-0144332. 99US-0144332. 99US-0144334. 99US-0144884. 99US-0144884. 99US-0144888. 99US-0144888. | 905-0145195 905-0145195 905-0145195 905-0145276 905-0145276 905-0145915 905-0145915 905-0145915 905-0146386 905-0146386 905-0147204 905-0147204 905-0147204 905-0147204 905-0147204 905-0147204 905-0147204 905-0147204 | 90S-0147410 90S-0147493 90S-01481793 90S-0148131 90S-014834 90S-014836 90S-014856 90S-014936 90S-014936 90S-014936 |
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| 7 | ** ** ** ** ** ** ** ** ** ** ** ** ** | : 8 | 2 |

990S-0151303 990S-0151303 990S-0151930 990S-0152363 990S-0152363 990S-0154018 990S-0154018 990S-0154019 990S-0155486 990S-0155486 990S-0155486 99US-0158029. 99US-0158232. 99US-0158369. 9908-0159294. 9908-0159294. 9908-0159295. 9908-0159330. 9908-0159331. 99US-0160980. 99US-0160981. 99US-0160989. 99US-0149902. 99US-0150566. 99US-0150884. 99US-0151065. 99US-0151066. 99US-0151066. 99US-0161404. 99US-0161405. 99US-0161359. 99US-0161360. 99US-0161360. 99US-0161920. 99US-0161992. 99US-0161993. 99US-0156596. 99US-0157117. 99US-0157753. 99US-0159637. 99US-0159584. 99US-0160741. 99US-0160768 99US-0160815 99US-0160770 99US-0160814 07-0cr-1999; 12-0cr-1999; 13-0cr-1999; 13-0cr-1999; 13-0cr-1999; 14-0cr-1999; 14-0cr-1999; 14-0cr-1999; 14-0cr-1999; 14-0cr-1999; 12-0cr-1999; 13-0cr-1999; 13-0cr-1999; 13-0cr-1999; 25-OCT-1999) 25-OCT-1999) 26-OCT-1999) 26-OCT-1999) 26-OCT-1999) 28-OCT-1999) 28-OCT-1999) 28-OCT-1999) 23-AUG-1999; 25-AUG-1999; 26-AUG-1999; 26-AUG-1999; 27-AUG-1999; 27-AUG-1999; 30-AUG-1999; 30-AUG-1999; 31-AUG-1999; 31-AU 23;

Gaps

DB 21; Length 433; 17; 156; Indels 135;

Query Match 7.3%; Score 169.5; DE Best Local Similarity 23.0%; Pred. No. 6e-07; Matches 105; Conservative 61; Mismatches 1

VVKDLRDD--PSAPTIEGMRKAGYPMAMFDENIJAPRKTLPIGPGTGPDDPKPVILLQLN 142

102 I-----DDFGDFAPTL-------NL-

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FIK-GGLILTVNGQHGAMDMVGQDAVIRLLSKA¢RNDPFTEEEMTAMNLDRKTIVPYLEN

143

FFKCGGASLGVGMQHHAADGFSGLHFINTWSDMAR

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LTIPPFIDRTLLRARDPPQPAFHHVEYQPAPSMKIPLDPSKSGPENTIVSIFKLTRDQLV 236
                                                                                                                                 ELKDAATKTLDASTKFVSTDDALSAFIWKSASRVRLERIDGSAPTEFCRAVDA----RPA 298
                                                                                                                                                                                                                                                                   GEIANESLGATASRLRSELDPASM 343
                                                                                                                                                                                                                                                                                                                                                                                                     403
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          --DVAGGDAVLTPVSASWAFFTFSPKAMS 242
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                                                                                                                                                                   237 ALK--AKSKEDGNTVSYSSYEMLAGHVWRSVGKAR--GLPNDQETKLYIATDGRSRLRPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant
                                                                                                                                                                                                                                                                                                                                                                                              344 RORTRGLATYLHNNPDKSNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGLGKPETVRRP
                                                                                                                                                                                                                                                                                                            : | | | : : : | | | LP-----PGYFGNVIFTATPLAVAGDLLSKPTWYAAGQIHDFLVRMDDNYLRSALD-
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7.3%; Score 169.5; DB 23; Length 433;
Best Local Similarity 23.0%; Pred. No. 6e-07;
Matches 105; Conservative 61; Mismatches 156; Indels 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 5; SEQ ID NO 2960; 261pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IFE ----PVESLMYFMPKKP-DGEFCAALSLRDEDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Herbicidally active polypeptide SEQ ID NO 2960.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Herbicidal; plant; agriculture; herbicide
                                                                                                                                                                                                                                                            MGVSNNYPGLLQNMTYHNSTI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB93749 standard; Protein; 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-AUG-2001; 2001WO-EP09892.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
YTIGPEVDHQIVKA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             useful as herbicides.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Weidler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-269010/31.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FARB ) BAYER AG.
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44 PIGASNFFDPQVMKEALSKALVPFYPMAGRLKRDDDGRIEIDCNGAGVLFVV--ADTPSV 101
                                                                                                                                                                                                                 GEIANESLGATASRLRSELDPASM 343
                                                                                                                                                                                                                                                           344 RORTRGLATYLHNNPDKSNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGLGKPETVRRP 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter
                                                                                                                                       VVKDLRDD--PSAPTIEGMRKAGYPMAMFDENIJAPRKTLPIGPGTGPDDPKPVILLQLN
                                                      --NL---ROLIPEVDHSAGIHSFPLLVLOVT
                                                                             143 FIK-GGLILTVNGQHGAMDMVGQDAVIRLLSKACRNDPFTEEEMTAMNLDRKTIVPYLEN
                                                                                                                         -- DVAGGDAVLTPVSASWAFFTFSPKAMS
                                                                                                                                                                    243 ELKDAATKTLDASTKFVSTDDALSAFIWKSASRVRLERIDGSAPTEFCRAVDA----RPA
                                                                                                                                                                                                                             : | | | : : : | | | LP-----PGYFGNVIFTATPLAVAGDLLSKPTWYAAGQIHDFLVRMDDNYLRSALD-
                                                                                                  -----GID----
                                                                                                                                                                                                                                                                          Arabidopsis thaliana protein fragment SEQ ID NO: 61175.
                                                                                                                                                                                                                                                                                                       IFE----PVESLMYFMPKKP-DGEFCAALSIRDEDM 434
                                                                                                                                                                                                                                                                                                                    139 FFKCGGASLGVGMQHHAADGFSGLHFINTWSDMAR-
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                                                                                                                                                                                                                                                                                                                                                                                    standard; Protein; 449
                                                                                                                                                                                                              299 MGVSNNYPGLLQNMTYHNSTI-
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99US-0132484.
99US-0132485.
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                                                      102 I-----DDFGDFAPTL-
                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                       202 YTIGPEVDHQIVKA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-FEB-2000;
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09-MAR-1999
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25-MAR-1999
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16-APR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                         AAG48444;
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23;

84

PIIVSTF--EQGLKR-FSEA-VPW--VAGQVKAEG----ISEGNTGTSFIVPFEDVPRV

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PR 06-WW-1899) 99US-013486.

PR 11-WM-1999) 99US-013421.

PR 14-WM-1999) 99US-013421.

PR 14-WM-1999) 99US-013421.

PR 14-WM-1999) 99US-0134321.

PR 14-WM-1999) 99US-0134321.

PR 19-WM-1999) 99US-0134321.

PR 20-WM-1999) 99US-0134321.

PR 20-WM-1999) 99US-0134321.

PR 20-WM-1999) 99US-0134321.

PR 20-WM-1999) 99US-013432.

PR 20-WM-1999) 99US-013432.

PR 20-WM-1999) 99US-013432.

PR 20-WM-1999) 99US-013442.

PR 10-WM-1999) 99US-013442.

PR 10-WW-1999) 99US-014433.

PR 10-WW-1
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990'S - 0151930 990'S - 0151930 990'S - 0153763 990'S - 0153758 990'S - 0154779 990'S - 0154779 990'S - 015478 990'S - 015486 990'S - 015658 990'S - 015659 990'S - 015765 990'S - 015765 990'S - 015765 990'S - 015765 990'S - 015786 990'S - 0158029 990'S - 0158029 990'S - 015929 99US-0150566. 99US-0150884. 99US-0151065. 99US-0151066. 99US-0145089.
99US-0145192.
99US-0145145.
99US-0145218.
99US-0145214.
99US-0145913.
99US-0145913.
99US-0145919.
99US-0145919. 99US-0147192. 99US-0147260. 99US-0147303. 99US-0151303 99US-0151438 99US-0147204 99US-0147302 99US-0147416 99US-0147493 99US-0147935 99US-0149175 99US-0149426 99US-0149930 99US-0151080 99US-0147038 99US-0148565 99US-0148684 99US-0149368 99US-0149902 99US-0146389 99US-0148171 99US-0148341 99US-0149722 99US-0149723 21-OCT-1999; 21-OCT-1999; 21-OCT-1999; 22 - 7UL - 1999; 23 - 7UL - 1999; 23 - 7UL - 1999; 23 - 7UL - 1999; 24 - 7UL - 1999; 27 - 7UL - 1999; 27 - 7UL - 1999; 28 - 7UL - 1999; 28 - 7UL - 1999; 28 - 7UL - 1999; 29 - 7UL - 1999; 20 - AUG - 1999; 30 - AUG - 1999; 40 - AUG - 1999; 65 - AUG - 1999; 66 - AUG - 1999; -OCT-1999; -OCT-1999; -OCT-1999;

us-10-614-954-6.rag

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446 AA;
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                                                                                                                     FALCO
                                    07-MAY-1999;
11-MAY-1999;
11-MAY-1999;
                                                               11-MAY-1999;
                                                                                                                                                                                                             Falco SC, 1
Thorpe CJ,
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                                                                                                                                                     (ODEL/)
(RAFA/)
(THOR/)
(SAKA/)
(WENG/)
                                                                                                                             (FAMO/)
(MEYE/)
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                                                                                                                                                                 23;
                                                                                                                                                                                                                                                                                                                                                                                                      403
                                                                                                                                                                                             192
                                                                                                                                                                                                                                                                                                       193 LTIPPFIDRTLLRARDPPQPAFHHVEYQPAPSMKIPLDPSKSGPENTTVSIFKLTRDGLV 252
                                                                                                                                                                                                                                                                                                                                        253 ALK--AKSKEDGNTVSYSSYEMLAGHVWRSVGKAR--GLPNDQETKLYIATDGRSRLRPQ 308
                                                                                                                                                                                                                    85 VVKDLRDD--PSAPTIEGMRKAGYPMAMFDENIIAPRKTLPIGPGTGPDDPKPVILLQLN 142
                                                                                                                                                                                                                                                                                            --- DVAGGDAVLTPVSASWAFFTFSPKAMS 242
                                                                                                                                                                                                                                                                                                                              ELKDAATKTLDASTKFVSTDDALSAFIWKSASRVRLERIDGSAPTEFCRAVDA----RPA 298
                                                                                                                                                                                                                                                                                                                                                                   -GEIANESLGATASRLRSELDPASM 343
                                                                                                                                                                                                                                                                                                                                                                                                                        -----RP 402
                                                                                                                                                                                                                                                         143 FIK-GGLILTVNGQHGAMDMVGQDAVIRLLSKACRNDPFTEEEMTAMNLDRKTIVPYLEN 201
                                                                                                                                                                                                                                                                                                                                                                            : | | | : : : | | | | LP-----PGYFGNVIFTATPLAVAGDLLSKPTWYAAGQIHDFLVRMDDNYLRSALD----
                                                                                                                                                                                 36 PIIVSTF--EQGLKR-FSEA-VPW--VAGQVKAEG-----ISEGNTGTSFIVPFEDVPRV
                                                                                                                                                                                                                                                                                                                                                                                                     RORTRGLATYLHINNPDKSINVSLTADADPSTSVMLSSWAKVGLWDYDFGLGLGKPETVRRP
                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plant; EST; expressed sequence tag; stress response; drought; heat; radiation; pathogen attack; grain flavour; disease resistance; peptide-methionine sulphoxide reductase; DNA repair; enzyme; intracellular protein transport.
                                                                                                                                                                Indels 135;
                                                                                                                                                                                                                                                                           -----GID----
                                                                                                                                              DB 21; Length 449;
                                                                                                                                                                                                                                                                                                                                                                                                                IFMGPGGIPYEGLSFVLPSPTNDGSLSVAIALQSEHM 439
                                                                                                                                                                                                                                                                                                                                                                                                                                        404 IFE-----PVESLMYFMPKKP-DGEFCAALSLRDEDM 434
                                                                                                                                             7.3%; Score 169.5; DB 21; 23.0%; Pred. No. 6.4e-07; Live 61; Mismatches 156;
                                                                                                                                                                                                                                                                         FFKCGGASLGVGMQHHAADGFSGLHFINTWSDMAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Corn stress response protein #10.
                                                                                                                                                               61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABUS8173 standard; Protein; 446
                                                                                                                                                                                                                                                                                                                                                                  MGVSNNYPGLLONMTYHNSTI-
                        990S-0160981.
990S-0160989.
990S-0161404.
990S-0161406.
990S-0161359.
                                                                                       990S-0161361.
990S-0161920.
990S-0161992.
990S-0161993.
99US-0160814.
99US-0160815.
99US-0160980.
                                                                                                                                                                                                                                      I-----DDFGDFAPTL-
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                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                          202 YTIGPEVDHQIVKA-
                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US2002152497-A1.
                                  22-0CT-1999;
25-0CT-1999;
25-0CT-1999;
25-0CT-1999;
26-0CT-1999;
        21-OCT-1999;
22-OCT-1999;
22-OCT-1999;
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28-OCT-1999;
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29-OCT-1999;
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                                                                                                                                                       Best Local Sim:
Matches 105;
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                                                                                                                                              Query Match
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ABU58173
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The invention relates to isolated nucleic acids encoding plant stress response proteins (including peptide-methionine sulphoxide reductases) appearing as ABU58148. ABU58246 (or a protein 80% identical to them) from Zea mays, Oryza sativa, Glycine max, or Triticum aestivum. Also included are expression cassettes, transformed host cells, transformed host cells, transformed host cells, transganic plants/seeds, modulating the level of peptide-methionine sulphoxide reductase in a plant and a computer system/data processing system for identifying, analysing, or modelling a genetic sequence. The plant nucleic acid is useful in developing strategies to improve plant response to stress (e.g. drought, heat, radiation or pathogen attack), engineering plants with increased disease and stress resistance, manipulating DNA repair and recombination efficiency, manipulating intracellular protein transport, and improvingly protecting grain flavour. The nucleic acids may also be used as probes or amplification primers in the detection, quantitation or isolation of enamenogens in preparing or screening antibachies, and in sense or immunogens in the proteins may be not more genes in a host cell, tissue or plant. The proteins may be simmunogens or antigens to obtain antibachies, and in sense or plant. The proteins may be used as immunogens or antigens to obtain antibachies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New peptide-methionine sulfoxide reductase and nucleic acids, useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              improving plant response to stress, engineering plants with increased disease and stress resistance, or and improving/protecting grain flavor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 plant. The proteins may be used as immunogens or antiyens to contain antibodies specifically immunoreactive with the protein, and in assays for enzyme agonists or antagonists. The present sequence is a plant stress response protein (or fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Odell JT, Rafalski JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.2%; Score 168.5; DB 24; Length 446;
21.8%; Pred. No. 7.8e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Meyers BC, Miao G,
Weng Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69 NTGTSFIVPFEDVPRVVVKDLRDDPSAPTIEG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Fig 4; 205pp; English.
                                                                                                99US-133042P.
99US-133427P.
99US-133428P.
                                                                                                                                                                                                                                              11-MAY-1999; 99US-133437P.
11-MAY-1999; 99US-133438P.
04-JUN-1999; 99US-137667P.
05-MAY-2000; 2000US-0566394.
19-FEB-2002; 2002US-0078929.
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ODELL J T.
RAFALSKI J A.
THORPE C J.
SAKAI H.
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Sakai H,
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ILLQLNFIK-GGLILTVNGQHGAMDMVGQDAVIRLLSKACRNDPFTEBEMTAMNLDRKTI 195
                                                       SELKDAATKTLDASTKFVSTDDALSAFIWKSASRVRLERIDGSAPTEFCRAVDARPAMGV
                                                                                                                             ---GLLQNMTYHNSTIGEIANESLGAT--ASRLRSELDPASMRQRTRGLATYLH
                                                                                                                                                ---OPPLPEGYFGNVIFTATPLANAGTVTAGVAEGASVIQAALDRMD-DGYCRSALDYLE
                                                                                                                                                                       356 NNPDKSNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGLGKPETVRRPIFE----PVES
                                                                                                                                                                                          ----RPVFMGPGGIAYEG
                                          ---SWAFFTFSPKAM
                                                                                                        250 VRLR-SQVPAREGAPRF-STYAVLAAHVWRCASLAR--GLPADQPTKLYCATDGRQRL--
                                                                                                                                                                                                                                                                                                                                                                       Plant, EST, expressed sequence tag, stress response, drought, heat, radiation, pathogen attack, grain flavour, disease resistance, peptide-methionine sulphoxide reductase, DNA repair, enzyme,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rafalski JA;
               143 LVLQVTHFKCGGVAIGVGMQHHVADGFSGLHFINSWADLCRGVPI
                                           -- PEVDHQIVKADVA-GGDAVLTPVSA-
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Weng Z;
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990S-133427P.
990S-133428P.
990S-133436P.
990S-133437P.
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2000US-0566394
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ODELL J T.
RAFALSKI J A.
THORPE C J.
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Sakai H,
                                           VPYLENYTIG-
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N-PSDB; ABX78348.
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FAMODU O O.
MEYERS B C.
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WENG Z.
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Thorpe CJ,
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11-MAY-1999
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(SAKA/)
(WENG/)
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(MEYE/)
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The invention relates to isolated nucleic acids encoding plant stress response proteins (including peptide-methiomine sulphoxide reductases) appearing as ABUS8148-ABUS8246 (or a protein 80% identical to them) from Zea mays, Oryza saltiva, Glycine max, or Triticum aestivum. Also included are expression casettes, transformed host cells, transgenic plants/seeds, modulating the level of peptide-methionine sulphoxide reductase in a plant and a computer system/data processing system for identifying, analysing, or modelling a genetic sequence. The plant modelec acid is useful in developing strategies to improve plant response to stress (e.g. drought, heat, radiation or pathogen attack); engineering plants with increased disease and stress resistance, manipulating DNA repair and recombination efficiency, manipulating DNA repair and recombination efficiency. The nucleic acids may also be used as probes or amplification primers in the detection, quantitation or isolation of gene transcripts, for recombinant expression of encoded polypeptions of immunogens in preparing or screening antibodies, and in sense or immunogens in a host for it the contraction of immunogens in a host for it that it issue or immunogens in a host for it that it issue or immunogens in a host for it that it issue or immunogens in a host for it that it issue or immunogens in a host for it that it issue or immunogens in a host for it that it issue or immunogens in a more contraction of income in immunogens in a more contraction of immunogens in a more contraction immunogens in a more contraction of immunogens in a more contraction of immunogens in a more contraction immunogens in a more genes in a more genes in a more contraction of immunogens in a more contraction immunogens in a more contraction immunogens in a more genes in a mor
                          New peptide-methionine sulfoxide reductase and nucleic acids, useful in improving plant response to stress, engineering plants with increased disease and stress resistance, or and improving/protecting grain flavor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   plant. The proteins may be used as immunogens or antigens to obtain antibodies specifically immunoreactive with the protein, and in assays for enzyme agonists or antagonists. The present sequence is a plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for enzyme agonists or antagonists. The stress response protein (or fragment).
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                                                                                                        TOISLLYPVSDSSQYPTIVSTFEQGLKRFSEAVPWVAGQVKAEGISEGNTGTSFIVPFED
                                                                                                                                                    SNVDLVVP---NFHTPSVYFYRPNGVSNFFDA-----KVMKEALSK-----VLVPFYP
                                                                                                                                                                                                           VPRVVVKDLRDDPSAPTI----EGMR--KAGYPMAMFDENIIAP----RKTLPIGPGTGP
                                                                                                                                                                                                                                                               ---MAARLRRDDDGRVEIYCDAQGVLFVEAETTAAIEDFGDFSPTLELRQLIPSVDYSAG
                                                                                                                                                                                                                                                                                                                       DDPKPVILLOLNFIK-GGLILTVNGQHGAMDMVGQDAVIRLLSKACRNDPFTEEEMTAMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               231 WAFFTFSPKAMSELKDAATKTLDASTKFVSTDDALSAFIWKSASRVRLERIDGSAPTEFC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LD-ISLPPFIDRTLLRARDPPLPVFDHIEYKPPPATKKTTPLQPSKPLGSDSTAVAVST-
                                                       Gaps
                                                       86;
  24; Length 439;
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                                   .06;
195; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                               LDRKTIVPYLENYTIG-----PEVDHQIVKADVA-
Query Match 6.9%; Score 161; DB Best Local Similarity 21.9%; Pred. No. 3.99-Matches 99; Conservative 72; Mismatches
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ABB93641 standard; Protein; 442 AA. RESULT 15 ABB93641 Д

18; | : | | : : | |: : | | : : | | : : | | : : | | : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : 230 223 VLTPVSASWAFFTFSPKAMSELKDAATKTLDASTKFVSTDDALSAFIWKSASRVRLERID 282 80 VNNHEDDIVSFYIDCDGLGAKFV--HAKAESIIVNDVLQSHGSVPY-----FISKFF 129 ------FHLSKRNILDLKAKANNEIDTNDLKISSLQAVVAYLMLSI--IRHSGLN 277 62 AEG-----ISEGNIGISFIVPFEDVPRVVVKD-LRDDPSAPTIEGMRKAGYPMAMF 111 DENIIAPRKTLPIGPGTGPDDPKPVILLQLNFIKGGLILTVNGQHGAMDMVGQDAVIRLL 171 SKACRN--DPFTE----EEMTAMNLDRKTIVPYLENYTI---GPEVDHQIVKADVAGGDA 222 283 GSAPTEFCRAVDARPAMG--VSNNYPGLLQNMTYHNSTIGEIANESLGATASRL----RS 336 337 ELDPA-----SMRQRTRGLATYLHNNPDKSNVSLTADADPSTSVMLSSWAKVGLW 386 61 24 KIHL-TPHDLDLLYLFYPQRGLLFHKPDPENSIIPRIMASLSTALEIY---FPFAGRLVK 79 4 KIQLDTLGQLPGLLSIYTQISLLY--PVSDSSQYPTIVSTFEQGLKRFSEAVPWVAGQVK 6.7%; Score 156.5; DB 23; Length 442; 21.1%; Pred. No. 1e-05; Live 68; Mismatches 174; Indels 101; Gaps 172

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Db 338 ETNESYEVPAKNWVRNVKRPKTSFGSRLANN------SLIISSSPRFEVY 381

Qy 387 DYDFGLGREFETVR 401

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Db 382 EHDF--GWGKPIAAR 394

Search completed: February 7, 2004, 23:40:47

JOB time : 554 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

7, 2004, 23:31:29; Search time 72 Seconds (without alignments) 265.031 Million cell updates/sec February Run on:

US-10-614-954-6 Perfect score:

1 MAFKIQLDTLGQLPGLLSIY......EDMDRLKADKEWTKYAQYVG 451 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

Searched:

328717 Total number of hits satisfying chosen parameters:

328717 seqs, 42310858 residues

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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/cgm2_6/prodata/1/iaa/eG_COMB.pep:*
/cgm2_6/prodata/1/iaa/PcTUS_COMB.pep:* Issued Patents AA:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result | | * Query | | | | |
|----------|--------|------------|--------|----|-------------------|-------------------|
| No. | Score | Match | Length | DB | ΠD | Description |
| \vdash | 2334 | 100.0 | 451 | 4 | US-09-538-414-6 | Sequence 6, Appli |
| a | 1860.5 | 79.7 | 459 | 4 | US-09-538-414-2 | N |
| m | 962.5 | 41.2 | 474 | 4 | US-09-538-414-8 | ìω |
| 4 | 4 | 6.1 | 448 | ĸ | US-09-457-046B-56 | 56 |
| Ŋ | | 6.1 | 436 | m | US-09-457-046B-62 | 62, |
| 9 | 3 | 5.7 | 448 | Н | US-08-207-904-2 | 2 |
| 7 | 134 | 5.7 | 448 | Н | US-08-207-904-17 | Sequence 17. Appl |
| 8 | 132 | 5.7 | 439 | æ | US-09-457-046B-28 | 28 |
| 6 | 130.5 | 5.6 | 451 | ٣ | US-09-457-046B-69 | 69 |
| 10 | • | 5.4 | 435 | æ | US-09-457-046B-60 | .09 |
| 11 | 125.5 | 5.4 | 439 | ო | US-09-457-046B-68 | 68 |
| Ŋ | 124 | 5.3 | 445 | m | US-09-457-046B-73 | 73, |
| m | 122 | 5.2 | 433 | ო | US-09-457-046B-66 | .99 |
| 4 | ä | 5.2 | 306 | m | US-09-457-046B-22 | 22, |
| N | 121.5 | 5.2 | 482 | m | US-09-457-046B-63 | |
| 9 | 118 | 5.1 | 450 | ٣ | US-09-457-046B-67 | 67 |
| 7 | 117 | 5.0 | 830 | 4 | US-09-562-737-34 | 34, |
| œ | 113 | 4.8 | 440 | æ | US-09-457-046B-45 | 4 |
| 6 | 1 | 4.8 | 441 | r | US-09-457-046B-54 | 54, |
| 20 | | 4.6 | 303 | ĸ | US-09-457-046B-20 | 20, |
| 21 | 105.5 | 4.5 | 446 | m | US-09-457-046B-74 | 74, |
| 22 | 105.5 | 4.5 | 3724 | N | US-08-804-227C-10 | 10, |
| m | 105.5 | 4.5 | 72 | (1 | US-08-804-198-4 | 4 |
| 4 | 104.5 | 4.5 | 33 | m | US-08-854-585-2 | 7 |
| D. | 4. | 4.5 | 1337 | 4 | US-09-447-533-2 | 7 |
| ٥ | | 4.5 | 33 | Ŋ | PCT-US95-05512-2 | 7 |
| 7 | 104 | 4.5 | 302 | ന | US-09-457-046B-24 | Sequence 24, Appl |

| Sequence 61, Appl | Sequence 4, Appli | 4 | 70. | 72. | 2, | Sequence 2, Appli | . 7 | 7 | 7 | 2 | 710 | Sequence 30777, A | Seguence 16967, A | Sequence 4, Appli | 4 | 4 | 4, 7 |
|-------------------|-------------------|-----------------|-------------------|-------------------|-----------------|-------------------|-----------------|------------------|-----------------|-----------------|--------------------|----------------------|----------------------|-------------------|-----------------|-----------------|-----------------|
| US-09-457-046B-61 | US-09-147-236-4 | US-09-522-474-4 | US-09-457-046B-70 | US-09-457-046B-72 | US-08-542-003-2 | US-08-322-760A-2 | US-09-236-949-2 | US-09-457-046B-2 | US-08-981-690-2 | US-09-455-777-2 | US-09-328-352-7107 | US-09-252-991A-30777 | US-09-252-991A-16967 | US-09-243-374-4 | US-07-876-280-4 | US-07-675-772-4 | US-08-063-170-4 |
| m | 4 | 4 | ო | m | Ŋ | C) | 4 | m | (7 | 4 | 4 | 4 | 4 | m | -1 | Н | Н |
| 458 | 802 | 802 | 461 | 455 | 1289 | 1289 | 1289 | 306 | 260 | 610 | 347 | 356 | 2482 | 446 | 1289 | 1289 | 1289 |
| 4.4 | 4.4 | 4.4 | 4.3 | 4.3 | 4.3 | 4.3 | 4.3 | 4.2 | 4.2 | 4.2 | 4.2 | 4.2 | 4.2 | 4.1 | 4.1 | 4.1 | 4.1 |
| 103.5 | 102 | 102 | 100 | 99.5 | 99.5 | 99.2 | 99.5 | 66 | 98.5 | 98.5 | 97 | 97 | 97 | 95.5 | 95 | 95 | 95 |
| 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 |

ALIGNMENTS

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Sequence (Application US/09538414)
Sequence (Application US/09538414)
Patent No. 6346655
GENERAL INFORMATION:
APPLICANT: Bolm. T.
APPLICANT: Reinders, J.
APPLICANT: Reinders, J.
APPLICANT: Reinders, J.
APPLICANT: Dill-Mackey, R.
TITLE OF INVENTION: Transgenic Plant and Methods;
FILE REFERENCE: sequencelist
CURRENT APPLICATION UNMBER: US/09/538,414
CURRENT FILING DATE: 2000-03-29
NUMBER OF SEQ ID NOS: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) ORGANISM: Fusarium graminearum
US-09-538-414-6
                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Ver. 2.0
US-09-538-414-6
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ô Gaps 0; tch 100.0%; Score 2334; DB 4; Length 451; al Similarity 100.0%; Pred. No. 5.5e-234; 451; Conservative 0; Mismatches 0; Indels 0 Query Match Best Local Similarity Matches 451; Conserv

180 61 KAEGISEGNIGISFIVPFEDVPRVVVKDLRDDPSAPTIEGMRKAGYPMAMFDENIIAPRK 120 120 180 240 241 MSELKDAATKTLDASTKFVSTDDALSAFIWKSASRVRLBRIDGSAPTEFCRAVDARPAMG 300 9 1 MAFKIQLDTLGQLPGLLSIYTQISLLYPVSDSSQYPTIVSTFBQGLKRFSEAVPWVAGQV 61 KARGISEGNICISFIVPFEDVPRVVVKDLRDDPSAPTIEGMRKAGYPMAMFDENIIAPRK 121 TLPIGPGTGPDDPKPVILLQLNFIKGGLILTVNGQHGAMDMVGQDAVIRLLSKACRNDPF 121 TLPIGPGTGPDDPKPVILLQLNFIKGGLILTVNGQHGAMDMVGQDAVIRLLSKACRNDPF 181 TEEEMTAMNLDRKTIVPYLENYTIGPEVDHQIVKADVAGGDAVLTPVSASWAFFTFSPKA 181 TEEEMTAMNLDRKTIVPYLENYTIGPEVDHQIVKADVAGGDAVLTPVSASWAFFTFSPKA 1 MAFKIQLDTLGQLPGLLSIYTQISLLYPVSDSSQYPTIVSTFRQGLKRFSEAVPWVAGQV g ਨੋ à d g d ð à δ

301 VSNNYPGLLQNMTYHNSTIGELANESLGATASRLRSELDPASMRQRTRGLATYLHNNPDK 360 241 MSELKDAATKTLDASTKFVSTDDALSAFIWKSASRVRLERIDGSAPTEFCRAVDARPAMG 300 셤 δ

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US-09-538-414-8
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                           420
                                                      420
301. VSNNYPGLLQNMTYHNSTIGEIANESLGATASRLRSELDPASMRQRTRGLATYLHNNPDK 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPDIELDIIGQQPPLLSIYTQISLVYPVSDPSQYPTIVSTLEEGLKRLSQTFPWVAGQVK 70
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                           SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGLGKPETVRRPIFEPVESLMYFMPKKPD
                                             Gaps
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                                                                                                                                                                                                                                                                     APPLICANT: Reinders, J.
APPLICANT: Kuznia, R.
APPLICANT: Kuznia, R.
APPLICANT: Kuznia, R.
TITLE OF INVENTION: Transgenic Plant and Methods
FILE REFERENCE: sequencelist
CURRENT APPLICATION NUMBER: US/09/538,414
CURRENT FILING DAIE: 2000-03-29
NUMBER OF SEQ ID NOS: 11
                                                                                  GEFCAALSIRDEDMDRIKADKEWIKYAQYVG 451
                                                                                                   || |::||||||||:|||||EFTASISLRDEDMERLKADEBWTKYAKYIG 459
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                                                                                                                                                                                                                                                                                                                                                                                                                                        ) ORGANISM: Fusarium sporotrichioides US-09-538-414-2
                                                                                                                                                                           ; Sequence 2, Application US/09538414; Patent No. 6346655; GENERAL INPORMATION:
A APPLICANT: Hohn, T.
APPLICANT: Salmeron, J.
APPLICANT: Peters, C.
APPLICANT: Kendra, D.
                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Ver. 2.0
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Best Local Similarity 77.65
Matches 349; Conservative
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LENGTH: 459
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US-09-538-414-2
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TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
CURRENT APPLICATION WHERE: US/09/457,046B
CURRENT APPLICATION NUBER: US/09/457,046B
CURRENT FILING DATE: 1999-12-07
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      141 GNTIGMAAKSGPVFAVQANFISGGLVLTIVGQHNIMDITGQESIINLINKSCHQKPFSDB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          357 NPDKSNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGLGKPETVRRPIFEPVESLMYFMP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 474;
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Pred. No. 2.9e-91;
84; Mismatches 158; Indels
                                                                                                                                     APPLICANT: Peters, C.
APPLICANT: Kendra, D.
APPLICANT: Reinders, D.
APPLICANT: Reinders, D.
APPLICANT: Reinders, R.
APPLICANT: Author Standa, R.
APPLICANT: Dill-MacKey, R.
TITLE OF INVENTION: Transgenic Plant and Methods
FILE REFERENCE: sequencelist
CURRENT APPLICATION NUMBER: US/09/538,414
CURRENT FILING DATE: 2000-03-29
NUMBER OF SEQ ID NOS: 11
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; Sequence 56, Application US/09457046B
; Patent No. 6287835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae
Sequence 8, Application US/09538414 Patent No. 6346655 GENERAL INFORMATION:
APPLICANT: Hohn, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41.2%;
44.4%;
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Best Local Similarity
                                                                                                                    APPLICANT: Salmeron,
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278 NLRGKVDSLCENTIGNMLSLMILKNEE--AAIERIQDVVDEI ---RRAKEIFSLNCKEMS 332
                                                                 ----MLSSWAKVGLWDYDFGLGLGKPETVRRPIFEPVE 409
                                                                                                  333 KSSSRIFELLEELGKVYGRGNEMDLWMSNSWCKLGLYDADF--GWGKPVWVTGRGTSHFK 390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----DELPLLFVQLTKFQCGGIALSFAISHAVVD--GQSALYFLTEWASLARGEP 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Version #1.25
                                                                                                                                            410 SLMYFMPKKPDGEFCAA-LSLRDEDMDRLKADKE 442
                                                                                                                                                                  DB 1;
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21.7%; Pred. No. 4
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/908,242
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CIBA-GEIGY Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/207,904
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US-08-207-904-2
; Sequence 2, Application US/08207904
; Patent No. 5477022
                                                               360 KSNVSLTADADPSTSV----
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Tuttle, AnnMarie
APPLICANT: Crossland, Lyle D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Lazar, Steven R. REGISTRATION NUMBER: 32,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: CC
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STATE: Ne
COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FTFSPKAMSELKDAATKTLDASTKFVSTDDALSAFIWKSASRVRLERIDGSAPTEFCRAV 293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DARPAMGVSNNYPGLLQNMTYHNSTIG------EIANESLGATASRLRSELDPASMR 344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GVSNNYPGLLQNMTYHNSTIGEIANESLGATASRLRSELDPASMRQRTRGLATYLHNNPD 359
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                                                                                                                                                                                 64
                                                                                                                                                                                                                    94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 62, Application US/09457046B
Patent No. 6287835
GENERAL INFORMATION:
FAPLICANT: Crotaou, Rodney et al.
TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
FILE REFERENCE: 53679
CURRENT APPLICATION NUMBER: US/09/457,046B
CURRENT FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                              5 IQLDTLGQLPGLLSIYTQISLLYPVSDSSQYPTIVSTFEQGLKRFSEAVPWVAGQVKAEG
                                                                                                                                                                                                     120 KTLPIGPGTGPDDPKPVILLQLNFIKGGLILTVNGQHGAMDMVGQDAVIRLLSKACRND-
                                                                                                                                                                                                                                                                                                -----DAQNASYEQLLF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             135 PVILLQLNFIK-GGLILTVNGQHGAMDMVGQDAVIRLLSKACRN-----DPFTE----
                                                                                                                                            Gaps
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                                                                                                                                          80;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           345 QRTRGLATYLHNNPDKSNVSLTADADPSTSVMLSSWAKVGLWDYDFGLG 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 3; Length 436;
                                                                                                  Length 448;
                                                                                              ; Score 142; DB 3; Length 44; Pred. No. 5.9e-06; 61; Mismatches 184; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.1%; Score 141.5; DB 3;
22.2%; Pred. No. 6.4e-06;
live 56; Mismatches 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      195 KPLDELPSKPMDRK------EEVEE--
                                                                                                                                                                                                                                                                                    | | ::||
95 NEELEVECTGEGALFVEALVDNDLSVLRDL-
                                                                                                6.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 6.1%
Best Local Similarity 22.2%
Matches 74; Conservative
                                                                                                                                      84; Conservative
                                       : Taxus cuspidata
                                                                                              Query Match
Best Local Similarity
                                                       US-09-457-046B-56
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-09-457-046B-62
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  448
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LENGTH: 44
TYPE: PRT
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                                     ORGANISM
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| Db 84 RLELDCNASGIVLMEAETEAKLDDLGDFSPSPDLNSLFPRVDYTI 128 Qy 123 PIGPGTGPDDPKPVILLQL-NFIKGGLILTTVNGQHGAMDMVGQDAVIRLLSKACRNDP 179 | 129 PIDELPILIFVQLTKFQCGGIALSFAISHAVVDGQSALYFLTEWASIARGEP | OY 180 FTEEBMTAMNLDRKTIVPYLENYTIGPEVDHQIVKADVAGGDAVLTPVSASW 231 | QY 232 AFFTESPKAMSELKDAATKTLDASTKEVSTDDALSAFIWKSASRVRL 278 : : : : : : : | QY 279 BRIDGSAPTEFCRAVDARPAMGVSNNYPGLLQNMTYHNSTIGEIANESLGATASRIRS 336 1 | QY 337 ELDPASMRQRTRGLATYLHNNPDKSNVSLTADADPSTSVMLSSW 380 DD 333AAIKMVTSDYANSTIDFLKNQEDLSKYQDIHAFRSKEGPFYGNPNLGVISW 383 QY 381 AKVGLWDYDFGLGLGKPFTVRRPIFEPVBSLMYFMP-KKPDGFFCAALSLRDEDMDRLK 438 DD 384 151.PILGLPGWGKBIHNSPGTHEYDGCVILFGKEGDGSLTVAILQAVHDAFK 439 | SULT 8 -09-457-046E Sequence 28, | GENERAL INFORMATION: , APPLICANT: Croteau, Rodney et al. , TITLE OF INFORTION: Transacylases of the Paclitaxel Biosynthetic Pathway | CURRENT APPLICATION UNMBER: US/09/457,046B CURRENT RILING DATE: 1999-12-07 NUMBER OF SEQ ID NOS: 74 ; SOFTWARE: Patentin Ver. 2.1 | ; SEQ 1D NO 28 ; LENGTH: 439 ; TYPE: PRT ; ORGANISM: Taxus cuspidata US-09-457-046B-28 | Query Match 5.7%; Score 132; DB 3; Length 439; Best Local Similarity 20.0%; Pred. No. 6.3e-05; Matches 90; Conservative 78; Mismatches 183; Indels 98; Gaps 21; | Qy 5 IQLDTLGQLPGLLSIYTQISLLYPVSDSSQYPTIVSTFEQGLKRFSEAVFWVAGQ 59 : :: : | QY 60 VKABGISEGNIGTSFIVPFEDVRVVVKDLRDDBSAPTIEGMRKAGYPMAMF 111 : | QY 112 DENIIAPRKTLPIGPGTGPDDPKFVILLQLNFIKGGLILTVNGQHGAMDMVGQDAVIKLL 171 | ADVAGGDAVLT | Db 180 AEMARGEVKLSLEPIWNRELVKLD-DPKYLQFFFFFFFRRAPSIVEKIVQ 227 Qy 226 PVSASWAFFTFSPKAMSELKDAATKTLDASTKFVSTDDALSAFIWKSASRVRLERIDGSA 285 | 228TYFIIDFETINYIKQSVMEECKEFCSSFEVASAMTWIARTRAFQIPESE | Qy 286 PTEFCRAVDARPAMGVSNNYPGILQNMTYHNS-†TIGEIANESLGATASRLRSELD 339 277 YVKILFGMDMRNSFNPPLPSGYYGNSIGTACAVDNVQDLLSGSLLRAIMIKKS 330 |
|---|--|---|--|--|--|--|---|---|---|---|---|---|---|--|---|--|--|
| | 221EBEKKNETKGSMLKLTKHQVEMLRKKANQGNQGRSYTRYBVYTAHIWRCACKARG | QY 279 ERIDGSAPTEFCRAVDARPAMGVSNNYPGLLQNMTYHNSTIGEIANESLGATASRLRS 336 276 HKFEQPTNLCICVNIRNIMQPPLPKSYFGNAIVDVIANGVSGDITSRPLEYVARRVR- 332 | Qy 337 ELDPASMRQRTRGLATYLHNNPDKSNVSLTADADPSTSVMLSSW 380 Db 333AAIXMVTSDYANSTIDPLKNQEDLSKYQDIHAFRSKEGPFYGNPMLGVISW 383 | OY 381 AKVGLWDYDFGLGLGKRETVRRPIFEPVESLMYFMP-KKPDGEFCAALSLRDEDMDRLK 438 | -17 Applicatic 5477002 FORMATION: | CE NVEN NVEN SEQU | Z 2 7 E | COUNTRY: USA ZIP: 10532 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible |) OPERATING SYSTEM: PC-DOS/MA-DOS) SOFTWARE: Patentin Release #1.0, Version #1.25) CURRENT APPLICATION DATA:) APPLICATION NUMBER: US/08/207,904) FILING DATE: | CLASSIFICATION: 800 ; PRIOR APPLICATION DATA: ; APPLICATION NUMBER: US/07/908,242 ; FILING DATE: | ; ATTORNEY/AGENT INFORMATION: ; NAME: Lazar, Steven R. ; REGISTRATION NUMBER: 32,618 ; REFERENCE/DOCKET NUMBER: CGC 1624 | ; TELECOMMUNICATION INFORMATION: ; TELERPHONE: (919)541-8615 ; TELEFAX: (919)541-8689 ; INFORMATION FOR SEQ ID NO: 17: | ਦੱ | ; MOLECULE TYPE: protein US-08-207-904-17 | Query Match 5.7%; Score 134; DB 1; Length 448; Best Local Similarity 21.7%; Pred. No. 4e-05; Marches 104: Conservative 58; Mismatches 183; Indels 134; Gaps 24; | 21 TOISILYPVSDSQYPTIVSTPRQGLKRF8EAVPWVAGQVKAEG 6 | IIKTIRTSLSKALVHFYPLSGRIRV VKDLRDDPSAPTIEGMRKAGYPMAMFDENI |

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Page

25; 211 435 340 PASMRQRTRGLATYLHNNPDKSNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGLGKPET 399 220 TDNVEERKKKKTIVVMLPLSTS-----QLQKLRSKANGSKHSDPAKGF-TRYETVTG 269 270 HVWRCACKARGH--SPEQPTALGICIDIRSRMEPPLPRGYFGNATLDVVAASTSGELISN 327 328 ELGFAASLISKAIKNVTNEYVMIĞI-EYLKNQKDLKKFQDLHALGSTEGFFYGNPNLGVV 386 ----AEGI----SEGNTGTSFIVPFEDVPRVVVKDLRDDPSAPTIEGMRKAGYPMA 109 -----LSDFKDFSPTPEFENL----- 119 MFDENIIAPRKTLPIGPGTGPDDPKPVILLQLNFIK-GGLILTVNGQHGAMDMVGQDAVI 168 120 MPQVNYKONPIETIPL------FLAQVTKFKCGGISLSVNVSHAIVD--GQSA-L 164 --IVKADVAGGDAVLTPVSASWAFFTFSPKAMSELKDAA--TKTLDASTKFVSTDDALSA 267 268 FIWKSASRVRLERIDGSAPTEFCRAVDARPAM--GVSNNYPGLLONMTYHNSTIGEIANE 325 -- DADPSTSVM 376 61 APPLICANT: Croteau, Rodney et al. TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway FILE REFERENCE: 53679 DILGQLPGLLSIYTQISLLYPVSDSSQYPTIVSTFEQGLKRFSEAVPWVAGQVK-----DQVGTITHIPTLY-----FYDKPSESFQGNVVEILKTSLSRVLVHFYPMAGRLRWLPRGR 377 LSSWAKVGLWDYDFGLGLGKPETVRRPIFEPVESLMYFMP-KKPDGEFCAALSLRDEDMD Gaps Indels 119; RLLS----KACRNDPFTEEEMTAMNLDRKTI----VPYLENYTIGPEVDHQ----Query Match 5.6%; Score 130.5; DB 3; Length 451; Best Local Similarity 21.7%; Pred. No. 9.4e-05; Matches 105; Conservative 64; Mismatches 195; Indels 119 326 SLGATASRLRSELDPASMRORTRGLATYLHNNPD-KSNVSLTA-421 ---PVQQQSALAMQNYFLFLKPSKNKPDG 409 CURRENT APPLICATION NUMBER: US/09/457,046B CURRENT FILING DATE: 1999-12-07 NUMBER OF SEQ ID NOS: 74 SEQ ID NO 69 LENGTH: 451 VRRPIFEPVESLM--YFM-----PKKPDG Sequence 69, Application US/09457046B Patent No. 6287835 GENERAL INFORMATION: 84 FELNCNAEGVEFIEAESEGK---; ORGANISM: Arabidopsis thaliana US-09-457-046B-69 RLK 438 AFK 444 -09-457-046B-69 ω 110 169 165 212 387 442 TYPE: PRT g DP à ð g à g à g à 임 à q à 셤 à 용 δ a B ₽

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57 AGOVKAEGISEGNIGISFIVPFEDVPRVVVKDLRDDPSAPTIEGMRKAGYPMAMFDENII 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117 APRKTLP-IGPGTGPDDPKPVILLQLNFI--KGGLILTVNGQHGAMDMVGQDAVIRLLSK 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                174 ACRNDPFTEEEMTAMNLDRKTIVPYLENYTIGPRVDHQIVKADVAGGDAVLTPVSASWAF 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----SRVRLERIDGSAPTEFCRAVDARPAMGVSNNYPGLLQNMTYHNSTIGEIA 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     270 QAMDIRLRIPSSVAPKDVIGNIQSGFSLKKDABSEFEI----PEIVATFRKNKERVNEMI 325
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              APPLICANT: Croteau, Rodney et al.
TTLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
FILE REFERENCE: 53679
CURRENT APPLICATION NUMBER: US/09/457,046B
CURRENT FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 60
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GENERAL INFORMATION:
APPLICANT: Croteau, Rodney et al.
TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
FITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
CURRENT APPLICATION NUMBER: US/09/457,046B
CURRENT FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 68
                                                                                                                                                                                                                                                                                                                                                                    4 KIQLDTLG-QLPGLLSIYTQISLLYP-VSDSSQYPTIVSTFEOGLK-----RFSEAVPWV
                                                                                                                                                                                                                                                                                                                                                                                                            ---VFSENLKLSLSETLSRFYP-L
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                                                                                                                                                                                                                                                                                 5.4%; Score 126.5; DB 3; Length 435; 20.2%; Pred. No. 0.00023; tive 77; Mismatches 182; Indels 133;
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23 RLQLSILDLYCPG---IXVSTIFFYDLITESSE---
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US-09-457-046B-68
Sequence 68, Application US/09457046B
Patent No. 6287835
                                                                                                                                                                                               TYPE: PRT
ORGANISM: Arabidopsis thaliana
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TYPE: PRT
ORGANISM: Catharanthus roseus
US-09-457-0468-68
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GENERAL INFORMATION:
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                                                                                                                                                                                LENGTH: 435
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286 BIKLIMPVDGRSRINNPSLPKGYCGNVVFLAVCTATVGDLSCNPLTDTAGKVQBALKGLD 345
                                                                                                                                                                                                                                                                                                       ---LRSELDPASMRQRTRGLATYLHNNPDKSNVSLTADADPSTSVMLSSWAKVGLWDYDF 390
                                                                                                                                                                                                                                                                                                                                              346 DDYLRSAIDHTESKP---GLPVPYMG8PEKTLY------PNVLVNSWGRIPYQAMDF 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIGPG--TGPDDPKPVILLQLNFIK-GGLILITVNGQHGAMDMVGQDAVIRLLSKACRNDP 179
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                                                                                             17 LSIYTQISLLYPVSDSSQYPTI-----VSTFRQGLKRFSEAVPWVAGQVKAEGISEGN 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FGLGL-GKPETVRRPIFEPVESLMYFMPKKPDGEFCAALS-LRDEDMDRLKADKEWTKY 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Croteau, Rodney et al.
TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
FILE REFERENCE: 53679
CURRENT APPLICATION NUMBER: US/09/457,046B
CURRENT FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70 TGTSFIVPFEDVPRVVVKDLRDDPSAPTIEGMRKAGYPMAMFDENI-----IAPRKTL
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                                                         SASWAFFTFSPKAMSELKDAATKTLDAS - - TKFVSTDDALSAFIWKSASRVRLERIDGSA
                                                                                                                                                                                                                                                                                                                                                                                                                                 391 GLGLGKPETVRRPIFEPVESLMY-----FMPKKP-DGEFCAALSLRDEDMDRLK 438
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L Similarity 20.3%; Pred. No. 0.00067;
97; Conservative 64; Mismatches 196; Indels 122;
                                                                                                                                                                                286 PTEFCRAVDARPAM---GVSNNYPGLLQNMTYHNSTIGEIANESLGATASR--
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Best Local S:
Matches 97,
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                                                                                                                                                                                                                                                                                                                                                                              134 KPVILLQINFIKGGLILTVNGQHGAMDMVGQDAVIRLLSK-----ACRNDPFTEEMTAM 188
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TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
FILE REPERENCE: 53679
CURRENT APPLICATION NUMBER: US/09/457,046B
CURRENT FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 74
SOFFWARE: Patentin Ver. 2.1
SEQ ID NO 73
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                                                                                                                                18 SIX---TQISLLYPVSDSSQYPTIVSTFEQGL-KRFSEAVPWVAGQVKAEGISEGNTGTS
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            Length 439;
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Best Local Similarity 19.6%; Pred. No. 0.00044;
Matches 93; Conservative 79; Mismatches 176;
      Query Match 5.4%; Score 125.5; DB 3; Best Local Similarity 20.5%; Pred. No. 0.0003; Matches 95; Conservative 75; Mismatches 193;
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GENERAL INFORMATION:
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US-09-457-046B-73
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              Sequence 22, Application US/09457046B
Batent No. 6287835
GENERAL INFORMATION:
APPLICANT: Croteau, Rodney et al.
APPLICANT: Croteau, Rodney et al.
TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
FILE REFERENCE: 53679
CURRENT APPLICATION NUMBER: US/09/457,046B
NUMBER OF SEQ ID DATE: 1999-12-07
SOFTWARE: PatentIn Ver. 2.1
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TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
FILE REPERENCE: 53679
CURRENT APPLICATION NUMBER: US/09/457,046B
CURRENT FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 74
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                                                                                                                                                                                                                                                                                                                                                                                                                    135 PVILLOLNFIKGGLILTVNGQHGAMDMVGQDAVIRLLSKACRNDPFTEEEMTAMNLDRKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30 SVSDLPMLSCHYIQKGCLF-TCPNLPLPALISHLKHSLSITLTHFPPLAGRLSTSSSGHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 TLGQLPGLLSIYTQISLLYPVSDSSQYPTIVSTFEQGLKRFSEAVPWVAGQVKAEG----
                                                                                                                                                                                                                                                                                                                                                                               69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.2%; Score 121.5; DB 3; Length 482; 19.5%; Pred. No. 0.00091; ative 76; Mismatches 204; Indels 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----KPPK--IVHTNNLIPCNIIAMAGSPRFPIYNNDFGWG 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           349 GLATYLHNNPDKSNVSLTADADPSTSVMLSSWAKVGLWDYDFGLG 393
                                                                                                                                                                                                                                                                                                                                       ; Score 121.5; DB 3; Length 3; Pred. No. 0.00042; 44; Mismatches 113; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLLAVQATKLKDGIALAITVNHAVADATSVWHFISSWAQLCK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            302 SNNYPGLLQNMTYHNSTIGEIANESLGATA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 63, Application US/09457046B Patent No. 6287835 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
CRGANISM: Arabidopsis thaliana
US-09-457-046B-63
                                                                                                                                                                                                                                                                                                                                   5.2%;
                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 20./*
Thes 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                             ORGANISM: Taxus cuspidata
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Best Local Similarity
Matches 99; Conserv
US-09-457-046B-22
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                                                                                                                                                                                                     SEQ ID NO 22
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LENGTH: 482
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112 DENIIAPRKTIPIGPGTGPDDPKPVILLQINFIKGGLILTVNGQHGAMDMVGQDAVIRLL 171
                       |:|| ::: |||
222 RERIFSFSRESIQELKAVVNKKKWLTVDNGEIDGVELLGKQSNDKLNGKENGILTEMLES 281
                                                                                                                                                                                                           ----DASTKFVSTD----DALSAFIWKSASRVRLERIDGSAPTEFCRAVDARPAMGVSN 303
                                                                                                                                                                                                                               360 KSNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGLGKPETVRRPIFEPVESLMYFMP-KK 418
                                                                    172 SKACRNDPFTEEEMTAMNLDRKTIVPYLENYTIGPEVDHQIVKADVAGGDAVLTPVSASW
                                                                                                     -----NTFAEVSRGAKNVTRQPDFT-RESVLISPAV----LKVP-QGGPKVTFDENAPL
                                                                                                                                                                                                                                                                              304 N---YPGLLQNM-TYHNSTIGEIANESLGATASRLRSELDPASMRQRTRGLATYLHNNPD
                                                                                                                                                                                                                                                                                                       340 NPEYFGNAIQSVPTF--ATAAEVLSRDLKWCADQLNQSV-AAHQDGRIRSVVADWEANP-
                                                                                                                                                                                                                                                                                                                                                                                                                                            :| ::| |::| |::| 478
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Search completed: February 7, 2004, 23:48:38 Job time: 73 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

7, 2004, 23:46:34; Search time 249 Seconds (without alignments) 379.243 Million cell updates/sec February Run on:

US-10-614-954-6 2334 Perfect score: Title:

1 MAFKIQLDTLGQLPGLLSIY......BDMDRLKADKEWTKYAQYVG 451 BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

801455 segs, 209382283 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Published_Applications_ Database

1: \cgg2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
\cgg2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
\cgg2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
\cgg2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
\cgg2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
\cgg2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
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\cgg2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:* /cgn2_6/ptodata/1/pubpaa/US60_NBW_PUB.pep:* /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | Annli | Appli | Appl: | Appl | Appl | Appl | | ۹ | Appl | Appl | Appl | Appl | Appl | Ann | App1 |
|--------------------------|-----------------|-----------------|-----------------|------------------|------------------|------------------|-------------------|-------------------|-------------------|------------------|------------------|-------------------|-------------------|------------------|------------------|
| | | | | | 52 | 60, | 200 | 56. | 56 | 56. | 56, | 62, | 62. | 2 | 62, |
| Description | Sequence 6. | Segmence | Seguence | Segmence | Segmence | Sequence | Seguence | | | Seguence | Seguence | | | | |
| QI | US-10-074-279-6 | US-10-074-279-2 | US-10-074-279-8 | US-10-078-929-64 | US-10-078-929-52 | US-10-078-929-60 | US-10-078-929-200 | US-09-866-572A-56 | US-09-866-570A-56 | US-10-166-984-56 | US-10-166-984-56 | US-09-866-572A-62 | US-09-866-570A-62 | US-10-166-984-62 | US-10-166-984-62 |
| DB | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 10 | 10 | 12 | 15 | 10 | 10 | 12 | 15 |
| Query Match Length DB | 451 | 459 | 474 | 436 | 446 | 439 | 431 | 448 | 448 | 448 | 448 | 436 | 436 | 436 | 436 |
| Query Match | 100.0 | 79.7 | 41.2 | 7.3 | 7.2 | 6.9 | 6.2 | 6.1 | 6.1 | 6.1 | 6.1 | 6.1 | 6.1 | 6.1 | 6.1 |
| Score | 2334 | 1860.5 | 962.5 | 170.5 | 168.5 | 191 | 144 | 142 | 142 | 142 | 142 | 141.5 | 141.5 | 141.5 | 141.5 |
| Result No. | Н | 2 | 3 | 4 | Ŋ | 9 | 7 | 6 0 | σ | 10 | 11 | 12 | 13 | 14 | 15 |

| | Appl | Appl | Appl | App1 | Appl | Appl | App1 | Appl | Appl | Appl | Appl | Appl | App1 | Appl | Appl | Appl | Appl | Appl | Appl | Appl | Appl |
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| | | | | | | | | | | . 60 | | | | | | | | | | | | | | | | | | | | 63, |
| | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence |
| | -09-866-572A-2 | -866-570A- | -99 | US-10-166-984-28 | -99 | -998-60- | -166- | -99 | - 1 | -998-60- | -10-166- | 10-166- | | US-09-866-570A-68 | -10-166- | -10-166- | | -998-60- | US-10-166-984-73 | -10-166- | -998-60- | -998-60- | -10-166-984-6 | -10-166-984- | US-09-866-572A-22 | -09-866-570A- | -10-166-9 | -10-166-9 | -60- | US-09-866-570A-63 |
| , | 0 | 10 | 12 | 15 | 10 | 10 | 12 | 15 | 10 | 10 | 12 | 15 | 10 | 10 | 12 | 15 | 10 | 10 | 12 | 15 | 10 | 10 | 12 | 15 | 10 | 10 | 12 | 12 | 10 | 10 |
| | 439 | 439 | 439 | 439 | 451 | 451 | 451 | 451 | 435 | 435 | 435 | 435 | 439 | 439 | 439 | 439 | 445 | 445 | 445 | 445 | 433 | 433 | 433 | 433 | 306 | 306 | 306 | 0 | 482 | |
| | | ٠. | 5.7 | ٠. | 5.6 | | | ٠. | ٠, | 5.4 | ٠. | 5.4 | 'n, | 'n, | 2 | 5. | ņ. | 'n | 5. | Š. | 'n. | Ŋ. | Ŋ. | Ŋ. | 'n | 'n | Ŋ. | ď. | 'n. | S. |
| | 132 | 132 | 132 | 132 | 130.5 | 130.5 | 130.5 | 130.5 | 126.5 | 126.5 | 126.5 | | 125.5 | 125.5 | 125.5 | 125.5 | 124 | 124 | 124 | 124 | 122 | 122 | 122 | 122 | 121.5 | 121.5 | 121.5 | 121.5 | 121.5 | 121.5 |
| , | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 |

ALIGNMENTS

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61 KAEGISEGNIGISFIVPFEDVPRVVVKDLRDDPSAPTIEGMRKAGYPMAMFDENIIAPRK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MAFKIQLDTLGQLPGLLSIYTQISLLYPVSDSSQYPTIVSTFBQGLKRFSBAVPWVAGQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MAFKIQLDTLGQLPGLLSIYTQISLLYPVSDSSQYPTIVSTFEQGLKRFSEAVPWVAGQV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 2334; DB 14; 100.0%; Pred. No. 3.7e-222;
                                                                                                                                                  APPLICANT: Reinders, J.
APPLICANT: Reinders, J.
APPLICANT: Ruznia, R.
APPLICANT: Lil-Mackey, R.
APPLICANT: Dill-Mackey, R.
TITLE OF INVENTION: Transgenic Plant and Methods
FILE REPERENCE: Sequencelist
CURRENT APPLICATION NUMBER: US/10/074,279
CURRENT FILING DATE: 2002-02-12
PRIOR PILING DATE: 2000-03-29
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                  Sequence 6, Application US/10074279; Publication No. US20020162136Al; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Fusarium graminearum
US-10-074-279-6
                                                                                                Salmeron, J.
Peters, C.
Kendra, D.
Reinders, J.
Kuznia, R.
Dill-Mackey, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 451; Conservative
US-10-074-279-6
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APPLICANT:
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SEGNICISFIVPFEDVPRVVVKDLRDDPSAPTIRGMRKAGYPMAMFDENIIAPRKTL-PI 124
                                                                                                                                            370 SVSLTADANPSSSIMLSSWAKVGCWEYDFGFGLGKPESVRRPKFEPFESLMYFWFKKPDG 429
250 SELKDAATKILDASSKFVSTDDALSAFIWQSTSRVRLARLDASTPTEFCRAVDMRGPMGV 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GNTIGMAAKSGPVFAVQANFISGGLVLTIVGQHNIMDITGQESIINLLNKSCHQKPFSDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    299 MGVSNNYPGLLONMIYHNSTIGEIANESLGATA$RLRSELDPA--SMRORTRGLATYLHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    357 NPDKSNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGLGKPETVRRPIFEPVESLMYFMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 380 CPDKTKVSIPQPIDTLSGIMVSSWAKVSLYDVDFNLGLGKPKSVRRPRFISLESLIYFMP
                                                                                                                     362 NVSLTADADPSTSVMLSSWAKVGLWDYDFGLGLGKPETVRRPIFEPVESLMYFMPKKPDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 QLDILGQQPSLYKLYTQICSIYRVPDPSAHDHIVNTLTRGLETLAKNPQWLAGNVVNBGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GPGTG-PDDPKPVILLQLNFIKGGLTLTVNGQHGAMDMVGQDAVIRLLSKACRNDPFTEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMTAMNLDRKTIVPYLENYTIGPEVD--HQIVKA--DVAGGDAVLTPVS-ASWAFFTFSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              239 KAMSELKDAATKTLDASTKFVSTDDALSAFIWK$ASRVRLERIDGSAPTEFCRAVDARPA
                                                             302 SNNYPGLLONMTYHNSTIGELANESLGATASRLREELDPASMRORTRGLATYLHNNPDKS
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44.4%; Pred. No. 2.98-86;
ive 84; Mismatches 158; Indels
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Balmeron, J.
APPLICANT: Balmeron, J.
APPLICANT: Beters, C.
APPLICANT: Reinders, J.
APPLICANT: Reinders, J.
APPLICANT: Reinders, J.
APPLICANT: Reinders, J.
APPLICANT: Ruznia, R.
APPLICANT: Ruznia, R.
APPLICANT: Ruznia, R.
APPLICANT: Ruznia, R.
APPLICANT: Ruznia, R.
APPLICANT: Ruznia, R.
APPLICANT: NUMBER: US/10/074,279
CURRENT APPLICATION NUMBER: US/09/538,414
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
                                                                                                                                                                                                                           430 EFTASISLRDEDMERLKADEEWTKYAKYIG 459
                                                                                                                                                                                                          451
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ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                   ; Sequence 8, Application US/10074279; Publication No. US20020162136A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match.
Best Local Similarity 44.4%;
Matches 202; Conservative (
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                                                                                                                     TEEEMTAMNLDRKTIVPYLENYTIGPEVDHQIVKADVAGGDAVLTPVSASWAFFTFSPKA
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                                    TLPIGEGTGPDDPKPVILLQINFIKGGLILTVNGQHGAMDMVGQDAVIRLLSKACRNDPF
        TLPIGPGTGPDDPKPVILLQLNFIKGGLILTVNGQHGAMDMVGQDAVIRLLSKACRNDPF
                                                                                           TEEEMIAMNLDRKTIVPYLENYTIGPEVDHQIVKADVAGGDAVLTPVSASWAFFTFSPKA
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US-10/0/4-2/9-2

US-10/0/4-2/9-2

Publication No. US20020162136A1

GENERAL INFORMATION:

APPLICANT: Boln, T.

APPLICANT: Reinfar, C.

APPLICANT: Reinfar, D.

APPLICANT: Reinfars, D.

APPLICANT: Reinfars, D.

APPLICANT: Reinfars, D.

APPLICANT: Reinfars, D.

APPLICANT: Reinfars, D.

APPLICANT: Reinfars, D.

APPLICANT: Ruznia, R.

CURRENT FILING DIVERTION: Transgenic Plant and Methods

FILE REFERENCE: sequencelist

CURRENT APPLICATION NUMBER: US/10/074,279

CURRENT FILING DATE: 2002-02-12

PRIOR FILING DATE: 2000-03-29
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Matches 349; Conservative
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324 NESLGATASRIRSELDPASMRQRTRGLATYLHNNPDKSNVSLTADADPSTSVMLSSWAKV 383
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                                                                                                                                                                                                                   Sequence 52, Application US/10078929
Publication No. US20020152497A1
                                                                                                                                                                                                                                                                                          Miao, Guo-Hua
Falco, Saverio Carl
Sakai, Hajime
                                                                                                                                                                                                                                                                      APPLICANT: Rafalski, Antoni
APPLICANT: Miao, Guo-Hua
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377 PMYDADFGWGAPR---
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Best Local Similarity
Matches 98; Conserv
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APPLICANT: Ridalski, Antoni
APPLICANT: Miao, Guo-Hua
APPLICANT: Falco, Saverio Carl
APPLICANT: Famodu; Omolayo O.
APPLICANT: Famodu; Omolayo O.
APPLICANT: Meyers, Blake
APPLICANT: Meyers, Blake
APPLICANT: Weng, Zude
APPLICANT: Weng, Zude
TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in
TITLE OF INVENTION: Stress Response
FILE REFERENCE: BB1357 US NA
CURRENT APPLICATION NUMBER: 120202-02-19
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                  417 KKPDGEFCAALSLRDEDMDRLKADKEWTKYAQYVG 451
                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: 09/566,394
                                                                                                                       Sequence 64, Application US/10078929
Publication No. US20020152497A1
GENERAL INFORMATION:
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ORGANISM: Triticum aestivum
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## APPLICANT: Falor, Saverio Carl
## APPLICANT: Falor, Saverio Carl
## APPLICANT: Famodu, Omolayo O.
## APPLICANT: Mengi, Joan T.
## APPLICANT: Mengi, Zude
## APPLICANT: Thorpe, Catherine
## APPLICANT: Thorpe, Catherine
## APPLICANT: Thorpe, Catherine
## APPLICANT: Thorpe, Catherine
## APPLICANT: Thorpe, Catherine
## APPLICANT: Wengi, Zude
## APPLICANTON NUMBER: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: Sample Number: S
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                                                                                                                                                                                  Indels 111;
                                                                                                                     384 GLWDYDFGLGLGKPETVRRPIFEPVESLMYFMPKKPDGEFCAALSLRDEDMD
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21.8%; Pred. No. 1.2e-07;
tive 63; Mismatches 177;
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GGDAVLTPVSAS 230

---RPIFMGP 396

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175 LD-ISLPPFIDRTLIRARDPPLPVFDHIEYKPPPATKKTTPLQPSKPLGSDSTAVAVST- 232
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                                                                                             DDPKPVILLQLNFIK-GGLILTVNGQHGAMDMVGQDAVIRLLSKACRNDPFTEEMTAMN 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  291 RAVDARPAM--GVSNNYPGLLQNMTYHNSTIGEIANESLGATASRLRSELDPASMRQRTR
                                                                                                                                                           127 IHSYPLLVLQVTYFKCGGVSLGVGMOHHVADGASGLHFINAWSDVAR
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FILING DATE: 2000-05-05
APPLICATION NUMBER: 60/133038
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APPLICATION UNMERS: 60/133042
FILING DATE: 1999-05-07
APPLICATION NUMBER: 60/133427
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APPLICATION NUMBER: 60/133437
FILING DATE: 1999-05-11
APPLICATION NUMBER: 60/133428
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APPLICATION NUMBER: 60/133436
FILING DATE: 1999-05-11
APPLICATION NUMBER: 60/137667
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PRIOR APPLICATION NUMBER: 60/137
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PRIOR PILING DATE: 1999-06-11
PRIOR PILING DATE: 1999-06-11
PRIOR PILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 208
SOFTWARE: MICROSOFT OFFICE 97
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Falco, Saverio Carl
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Thorpe, Catherine
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US-10-078-929-200
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Thorpe, c.
Zude
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Publication No. US20
GENERAL INFORMATION:
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                                                                           242 SELKDAATKTLDASTKFVSTDDALSAFIWKSASRVRLERIDGSAPTEFCRAVDARPAMGV 301
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TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in
TITLE OF INVENTION: Stress Response
FILE REFERENCE: BB1357 US NA
FILE REFERENCE: BB1357 US NA
CURRENT APPLICATION NUMBER: US/10/078,929
CURRENT FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: 09/566,394
                                                                                                                     356 NNPDKSNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGLGKPETVRRPIFE-----PVES
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PRIOR APPLICATION NUMBER: 60/137667
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Publication No. US20020152497A1
GENERAL INFORMATION:
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APPLICATION NUMBER: 60/133038
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PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: 60/133427
PRIOR FILING DATE: 1999-05-11
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PRIOR FILING DATE: 1999-05-11
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PRIOR APPLICATION NUMBER: 60/133438
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Falco, Saverio Carl
Sakai, Hajime
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Odell, Joan T.
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NUMBER OF SEQ ID NOS: 208
SOFTWARE: Microsoft Office 97
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Thorpe, Catherine
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ORGANISM: Glycine max
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Best Local Similarity
Matches 99; Conserv
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US-10~078-929-60
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95 NEELEVECTGEGALFVEALVDNDLSVLRDL-
       DARPAMGVSNNYPGLLQNMTYHNSTIG-
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SOFTWARE: PatentIn Ver. 2.1
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ORGANISM: Taxus cuspidata
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344 LRSRIVA-
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US-10-166-984-56
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                                                                                                                                                                                                                                                                                                                                                            403
                                                                                                                                                                 180 LSVAIPPFIDRTLIRA---RDPPTPAFEHSEYDQPPKL--KSVPESKRGS-----SAS 227
                                                                                                                                                                                                               WAFFTFSPKAMSELKDAATKTLDASTKFVSTDDALSAFIWKSASRVRLERIDGSAPTEFC 290
                                                                                                                                                                                                                                                                                                                         332
                                                                                                                                                                                                                                                                                                                                                                             333 DEYLRSALDFLECQPDLSKLIRGSNYFASPNLNINSWTRLPVHESDFGWG-----RP 384
                                                                     119 RKTLPIGPGTGPDDPKPVILLQLNFIK-GGLILTVNGQHGAMDMVGQDAVIRLLSKACRN 177
                                                                                                      RKFIPTVDTSGDISSFPLIIFQVTRFKCGGVCLGTGVFHTLSDGVSSLHFINTWSDMARG 179
                                                                                                                                                                                                                                                                                   291 RAVDAR----PAMGVSNNYPGLLQNMTYHNSTI----GEIANESLGATASRLRSELDPASM 343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           137 -SLP--PNIQVQDLHPLILQVTRFTCGGFVVGVGFHHGICDARGGTQFLQGLADMARGET 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -PFTEREEMTAMNLDRKTIVP---YLENYTIGPEVDHQIVKADVAGGDAVLTPVSASWAF 233
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TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
TITLE OF INVENTION NUMBER: US/09/866,572A
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 09/457,046
PRIOR FILING DATE: 1999-12-07
                                                                                                                                         ----DPFTEEEMTAMNLDRKTIVPYLEN--YTIGPEVDHQIVKADVAGGDAVLTPVSAS
                                                                                                                                                                                                                                                                                                                      279 VATDGRSRLCPPLP----PGYLGNVVFTATPMAESGELQSEPLTNSAKRIHSALSRMD-
                                                                                                                                                                                                                                                                                                                                                         344 RORTRGLATYLHNNPDKSNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGLGKPETVRRP
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                                      56;
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   DB 14; Length 431;
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                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     194 KPLVEPVW-----NRELIKPEDLMHLQFHKFG--LIRQPLKLD-
   ; Score 144; DB 14; I
; Pred. No. 3e-05;
48; Mismatches 153;
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20.5%; Pred. No. 5
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6.2%;
ilarity 24.6%;
Conservative 48
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Best Local Similarity 20.5%
Matches 84; Conservative
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SOFTWARE: PatentIn Ver. 2.1
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                Similarity
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US-09-866-572A-56
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                                  84;
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LENGTH: 448
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 Query Match
Best Local
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----EIANESLGATASRLRSELDPASMR 344
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Patent No. US20020168745A1

GENERAL INFORMATION:

APPLICANT: Croteau, Rodney et al.

TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
FILE REFERENCE: 53679

CURRENT FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: US/09/467,046B

PRIOR FILING DATE: 1999-12-07
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Publication No. US20040005562A9

GENERAL INFORMATION:

APPLICANT: Croteau, Rodney et al.

TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway

FILE REFERENCE: 4630-62267

CURRENT PAPLICATION NUMBER: US/10/166,984

CURRENT FILING DATE: 2002-06-10

PRIOR APPLICATION NUMBER: US 09/866,570
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6.1%; Score 142; DB 10; Length 4
Best Local Similarity 20.5%; Pred. No. 5.1e-05;
Matches 84; Conservative 61; Mismatches 184; Indels
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us-10-614-954-6.rapb

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179
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ITLE REFERENCE: 4630-6226,
CURRENT FILING DATE: 2002-06,984

CURRENT FILING DATE: 2002-06,70

PRIOR APPLICATION NUMBER: US 09/866,570

PRIOR APPLICATION NUMBER: US 09/866,570

PRIOR PILING DATE: 2001-05-25

PRIOR FILING DATE: 1999-12-07

PRIOR FILING DATE: 1999-12-07

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PRIOR FILING DATE: 1999-12-07
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20.5%; Pred. No. 5.1e-05;
tive 61; Mismatches 184; Indels
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1 Similarity 20.5%; Pred No. 5.1e-05;
84; Conservative 61; Mismatches 184;
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PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 09/457,046
PRIOR FILING DATE: 1999-12-07
PRIOR FILING DATE: 1999-12-07
PRIOR FILING DATE: 1999-09-30
NUMBER OF SEQ ID NOS: 76
SOFTWARE: PATCHIN Ver. 2.1
SEQ ID NO 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 56, Application US/10166984; Publication No. US20030108891A1; GENERAL INFORMATION:
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US-10-166-984-56
                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Taxus cuspidata
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Best Local Similarity
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Best Local Similarity
Matches 84; Conserv
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US-10-166-984-56
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Patent No. US20020138859A1
GENERAL INFORMATION:
APPLICANT: Croteau, Rodney et al.
TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
FILE REFERENCE: 53679
CURRENT APPLICATION NUMBER: US/09/866,572A
CURRENT PILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 09/457,046
PRIOR APPLICATION NUMBER: 09/457,046
SROG ID NOS: 74
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 62
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                                  35 LQLSAVDRLPGMKFATFSAVLVYNASSHSIFANPAQIIRQALSKVLQYYPAFAGRIRQKE
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IQLDTLGQLPGLLSIYTQISLLYPVSDSSQYPTIVSTFEQGLKRFSEAVPWVAGQVKAEG
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22.2%; Pred. No. 5.5e-05;
tive 56; Mismatches 133;
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195 KPLDELPSKPMDRK-
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SEQ ID NO 62
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Sequence 62, Application US/10166984

Sequence 62, Application US/10166984

Publication No. US20040005562A9

GENERAL INFORMATION: Transacylases of the Paclitaxel Biosynthetic Pathway

TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway

TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway

TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway

CURRENT APPLICATION NUMBER: US 10/10/166,984

CURRENT FILING DATE: 2002-06-10

PRIOR FILING DATE: 1999-12-07

PRIOR FILING DATE: 1999-12-07

PRIOR FILING DATE: 1999-09-30

NUMBER OF SEQ ID NOS: 76

SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                 Sequence 62, Application US/09866570A
Patent No. US20020168745A1
GENERAL INFORMATION:
APPLICANT: Croteau, Rodney et al.
TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
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                               410 SIMYFMPKKPDGEFCAA-LSLRDEDMDRLKADKE 442
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         410 SLMYFMPKKPDGEFCAA-LSLRDEDMDRLKADKE
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CURRENT APPLICATION NUMBER: US/09/866,570A
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US/09/457,046B
PRIOR FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentin Ver, 2.1
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135 PVLLIQANFFSCGGLVITICVSHKITDATSLAMFIRGWAESSRGLGITLIPSFTASEVFP 194
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TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
FILE REPERENCE: 4630-62267
CURRENT APPLICATION NUMBER: US/10/166,984
CURRENT FILING DATE: 2002-06-10
PRIOR PELICATION NUMBER: US 09/866,570
PRIOR FILING DATE: 2001-05-25
PRIOR PELICATION NUMBER: US 09/457,046
PRIOR FILING DATE: 1999-12-07
PRIOR FILING DATE: 1999-12-07
PRIOR FILING DATE: 1999-12-07
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                                                                                                                          Query Match 6.1%; Score 141.5; DB 12; Length Best Local Similarity 22.2%; Pred. No. 5.5e-05; Matches 74; Conservative 56; Mismatches 133; Indels
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TYPE: PRT
ORGANISM: Arabidopsis thaliana
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ORGANISM: Arabidopsis thaliana
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Best Local Similarity 22.2's
Matches 74; Conservative
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227 KIKKLRAKASRNL---VKNPTRVEAVTALFWRCVTKV--SRLSSLTP----RTSVLQILV 277

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BI191800 12f11fs.r
BI191865 13b10fs.r
                   7, 2004, 18:04:23; Search time 3189 Seconds (without alignments) 10334.547 Million cell updates/sec
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Maximum Match 100%
Listing first 45 summaries
OM nucleic - nucleic search, using sw model
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BI947129
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Gapop 10.0 , Gapext 1.0
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em_gss_mam:*
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Maximum DB seq length: 2000000000
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Match Length DB
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Wing, R., Muchbauer, G.J., Close, T.J., Kleinhofs, A., Wise, R., Heinen Wing, R., Muchbauer, D., Yu, Y., Henry, D., Palmer, M., Rambo, T., S., Begum, D., Fersch, D., Yu, Y., Henry, D., Palmer, M., Choi, D.W., Oates, R. and Main Simmons, J., Fenton, R.D., Malatrasi, M., Choi, D.W., Oates, R. and Main
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Štreptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST 19-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        709 AACTATACGATTGGCCCCCGGGTAGATCATCAGATTGTCAAACCTGATGTAGCTGGGTGG 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        650 ACCGAAGAAATGACGGCCATGAACCTCGATCGCAAGAACGATAGTTCTTACCTTG-A 708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 769 GIGACGCTGICTCACGCCGGTCAGTGCAAGCTGGGGCGTCTTCACATTCAGCCC-AGGC 827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Development of a genetically and physically anchored BST resource for barley genomics: Fusarium infected Morex spike cDNA library Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST library HVcDNA0012
                                                                                                                                                                                                               661 GACGCTGT-TCTCACGCCGGTCAGTGCAAGCTGGGCGTTCTTCACATTCAGCCCCAAGGC
ACGITACCIATIGGACCIGGIACIGGICCCGACGACCCAAAGCCIGIAAITCIAIIGCAG
                                                      470 ACGITACCIATIGGACCIGGIACIGGICCCGACGACCCAAGCCIGIAAITCIAIIGIA
                                                                                                                                                                                                                                                                                                 481 ATGGTAGGCCAAGATGCGGTGATCCGTCTACTCTCCAAGGCGTGCCGTAACGACCCATTC
                                                                                                                                                                                                                                                                                                                                                                   601 AACTATACGATTGGCCCCCGAGGTAGATCATCAGATTGTCAAAGCTGATGTAGCTGGTGGT
                                                                                                                                                    CTCAACTTCATCAAGGGGGGGACTCATCCTCACTGFCAACGGACAGCACGGTGCTATGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                     541 ACCGAAGAGAAATGACGGCCATGAACCTCGATCGCAAGACGATAGTTCCTTACCTTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HISWELLO03NIOF Hordeum vulgare spike EST library HVcDNA0012 (Fusarium infected) Hordeum vulgare subsp. vulgare cDNA clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          828 CATGTCANAGCTC-AGGATGCTGCTACCAGAACTCT 862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clemson University
1100 Jordan Hall, Clemson, SC 29634, USA
TTel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab_host="TJC121"
/clone lib="Hordeum vulgare
(Fusarium infected)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total hg bases = 147
Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence stoart: 5
High quality sequence stop: 668.
Location/Qualifiers
is 1.1055
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HVSME10003N10f, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/cultivar="Morex"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: rwing@clemson.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BI947129.1 GI:16286403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BI947129
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BI947129
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: pBluescript SK(-); Site 1: ECORI; Site 2: XhOI; Plants were grown at the University of Minnesota in the GJ Muchlbauer lab; spikes were harvested and snap frozen at 0, 12, 3, 4, 5, 6, and 8 days after Fusarium graminearum incoulation (Heinen). In the TU Close lab at the University of California, Riverside, total RNA was prepared from each sample pool, equal quantities of all eight RNA pools were combined, poly(A) RNA was purified from the mixture, one primary unamplified cDNA library was made, and I million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids (Choi, Fenton, Malatrasi). Phagemids were placed and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Nature).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see close TJ, Wing R, Kleinhoffs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)" 262 c 204 g 209 t lothers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clone_lib="Hordeum vulgare spike EST library HVcDNA0012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCTICGAGCAAGGICTTAAAGGGCTTCTCCGAAGCCGTCCCATGGGTCGCAGGCCAGGTC
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                                                                                                                                                                                                                                                                                     'organism="Hordeum vulgare subsp. vulgare"
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ilarity 95.8%; Pred. No. 6.9e-178;
Conservative 0; Mismatches 28;
                                                      Email: rwing@clemson.edu
Total hq bases = 598
Seq primer: AATTAACCTCACTAAAGGG
High quality sequence stop: 755.
                                                                                                                                                                                                                                                                                                                                                                                              db_xref="taxon:112509"
clone="HVSME10014017f"
tissue_type="Spike"
lab_host="TJC121"
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                                                                                                                                                                                                               Location/Qualifiers
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cultivar="Morex"
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/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhOI; Plants were grown at the University of Minnesota in the GY Muchbauer lab; spikes were harvested and snap frozen at 0, 1, 2, 3, 6, and 8 days after Fusarium graminearum inoculation (Heinen). In the TU Close lab at the University of California, Riverside, total RNA was prepared from each sample pool, equal quantities of all eight RNA pools were combined, poly(A) RNA was purified from the mixture, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) CDNA phagemids (Choi, Fenton, Malatrasi). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Akkins and Ming). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or environ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  421 CiridgAAIAGGCCCTCTACGGCCGCTCCAAAAAAGCAAGGTTGGCCCCTACCGAGTTC 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence analysis see
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Matches 481; Conservative
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Eukaryota; Fungl; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium. 1 (bases 1 to 512)
Ren.Q., Tag.A., Peplow,A., Lai,H., Kupfer,C., Peterson,A., Beremand, M. and Roe,B.
Analysis of a Fusarium sporotrichioides EST database
                                                                                                                                                                           EST 10-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:5514"
/clone="12f11fs"
/clone_lib="Fusarium sporotrichioides Tri 10 overexpressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: pBlueScript SK-; Site_1: EcoR1; Site_2:
Xhol; 5' and of cDNA cloned into EcoR1 site of pBluescript
i 3' end of CDNA cloned into XhoI site of pBluescript"
i 153 c 121 g 107 t 1 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact Dr. Marian Beremand regarding clone availability Included is the best homolog from a blastx search of Genbank nr 04-09-01 871 8e-94 gi|4378882|gb|AAD197 (AF127176)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        196 GACCGAGGGCATCAGCGAAGGAAACACAGGAACTTCCAAGATCATTCCATATGAGGAGAC 255
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                                                                                                                                                                                     12f11fs.rl Fusarium sporotrichioides Tri 10 overexpressed cDNA library Fusarium sporotrichioides cDNA clone 12f11fs 5', mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Ovall, Norman, OK 73019, USA
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Pred. No. 8.8e-90;
0; Mismatches 88; Indels 0;
                                                                                                                                                                           linear
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/organism="Fusarium sporotrichioides"
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Fusarium sporotrichioides
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                                                                                                                                                                                                                                                                BI191800
BI191800.1 GI:14665479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 405 325 4912
Fax: 405 325 7762
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Fax: 405 325 7762
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XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript
; 3' end of cDNA cloned into XhoI site of pBluescript"
151 c 122 g 106 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
1 (bases 1 to 508)
Ren, Q., Tag, A., Peplow, A., Lai, H., Kupfer, C., Peterson, A., Beremand, M. and Roe, B.
Analysis of a Fusarium sporotrichioides EST database
Unpublished
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/clone_lib="Fusarium sporotrichioides Tri 10 overexpressed
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13b10fs.rl Fusarium sporotrichioides Tri 10 overexpressed cDNA
library Fusarium sporotrichioides cDNA clone l3b10fs 5', mRNA
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Tex: 405 325 74912
Email: broe@ou.edu
Contact Dr. Marian Beremand regarding clone availability Included
is the best homolog from a blastx search of Genbank nr 04-09-01
857 3e-92 gi 4378882 jgb) AAD197 (AF127176)
                                                                                                                                                         435
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                                                            GAGAAAGGCGGGATACCCTATGGCGATGTTTGACGAGAACATCATCGCGCCAAGGAAGAC
          256 ACCCGGTCTTGTGGTGAAAGACCTCCGTGATGATTCCTCAGCGCCAACGATCGAGGGGTT
                                                                                        GAGAAAGGCGGGTTTCCCCCTTAGAGATGTTTGACGAGAACGTCGTCGCTCCGAGGAAGAC
                                                                                                                                               GITACCTATTGGACCTGGTACTGGTCCCGACGACCAAAGCCTGTAATTCTATTGCAGCT
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Fusarium sporotrichioides
Eukaryota: Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Other ESTS: 13b10fs.fl
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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Location/Qualifiers
1. 508
/organ="Fusarium sporotrichioides"
/mol type="mRNA"
/strain="Tri 10"
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Best Local Similarity 81.8%; Pred. No. 7.2e-89;
Matches 405; Conservative 0; Mismatches 90;
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Eukaryota; Fungi; Ascomycotales; mitosporic Hypocreales; Fusarium.

1 (bases 1 to 498)
Ren, Q., Tag, A., Peplow, A., Lai, H., Kupfer, C., Peterson, A., Beremand, M. and Roe, B.
Analysis of a Fusarium sporotrichioides EST database
Unpublished
Contact: Bruca. Roe, University of Oklahoma, broe@ou.edu
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
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Contact broe@ou.edu
Contact Dr. Marian Beremand regarding clone availability Included
Contact Dr. Marian Beremand regarding clone availability Included
is the best homolog from a blastx search of Genbank nr 04-09-01
is the best homolog from a blastx search of Genbank nr 04-09-01
trichothecema3-0-acetyltransfer
                                                                                                                    CITCGAGCAAGGICITAAGCGCTICTCCGAAGCCGTCCCATGGGTCGCAGGCCAGGTCAA 182
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                             CCAGATCAGTCTGGTTTACCCCGTCTCTGATCCCTCCAGTATCCCACCATCGTCAGCAC 132
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CCAAATCAGICTCCTTAACCCCGTCTCTGATICCTCTCAAIAICCCACIAIIGICAGCAC
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/mol_type="mRNA"
/strain="Tri 10"
/db_xref="taxon:5514"
/clone="01e06fs"
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High quality sequence stop: 476.
Location/Qualifiers
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Fusarium sporotrichioides
Fusarium sporotrichioides

Eukarycta; Fusarium.

1 (bases 1 to 499)
S Ren, Q., Tag, A., Peplow, A., Lai, H., Kupfer, C., Peterson, A., Beremand, M. and Roe, B.
Analyais of a Fusarium sporotrichioides EST database
Unpublished
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
G20 Parrington, Oyal, Norman, OK 73019, USA
                                  /note="Vector: pBlueScript SK-; Site 1: EcoR1; Site 2: Xho1; 5' end of cDhA cloned into EcoR1 site of pBluescript; 3' end of cDhA cloned into XhoI site of pBluescript" 156 c 113 g 109 t
/clone lib="Fusarium sporotrichioides Tri 10 overexpressed
cDNA library"
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                                                                                                                                                                                                                         TCATCCTCACTGTCAACGGACAGCACGGTGCTATGGATATGGTAGGCCAAGATGCGGTGA
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11f11fs.fl Fusarium sporotrichioides Tri 10 overexpressed cDNA
1ibrary Fusarium sporotrichioides cDNA clone l1f11fs 3', mRNA
                                                                                                                                                                                        3;
                                                                                                                                                   DB 12; Length 498;
                                                                                                                                               Score 323.4; DB 12; Length
Pred. No. 5.2e-81;
0; Mismatches 101; Indels
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79.2%;
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Fax: 405 325 7762
                                                                                                                                                                 Local Similarity
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                                                                                                            ORIGIN
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/note="Vector: pBlueScript SK-; Site_1: EcoRI; Site_2: XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript i 3' end of cDNA cloned into XhoI site of pBluescript" a 136 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tri 10 overexpressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGGCGAAATCGCCAACGAGTCACTCGGCGCAACAGCATCACGCCTTCGTTCAGAACTCGA 1016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCCCGCGAGCATGCGCCAGCGAACAAGAGGTCTCGCGACGTACCTGCACAACAACAACCGGA 1076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1137 TTGGGCCAAGGTGGGACTCTGGGATTACGACTTTGGGCTCGGACTGGGTAAGCCCCGAGAC 1196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1316
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13b10fs.fl Fusarium sporotrichioides Tri 10 overexpressed cDNA
library Fusarium sporotrichioides cDNA clone 13b10fs 3', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          439 CGCCGAAATCGCCAACGAACCACTTGGCGCAACAGCATCACGCTCGCGCTCGGAACTCAA 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                140
Email: broe@ou.edu
Contact Dr. Marian Beremand regarding clone availability Included
is the best homolog from a blastx search of Genbank nr 04-09-01
is the best homolog from a blastx search of Genbank nr 04-09-01
se folsofelsona-0-acetyltransfer
Seq primer: M13-20
High quality sequence stop: 428.

Location/Qualifiers
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Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
1 (bases 1 to 481)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               319 CAAGTCGAGCGTCTCCCTGACCGCCGATGCGAATCCGTCAAGCAGCATCATGCTGAGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1197 IGTGAGACGGCCAATCTTTGAGCCTGTTGAGGCTTGATGTACTTTATGCCCAAGAAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      199 TGTGAGAAGACCTCTGGAACCTTTGAGAGTTTGATGTACTTTATGCCCAAGAAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1257 TGATGGCGAGTTCTGTGCGGCGCTTTCTCTGAGGGATGAGGATATGGACCGATTGAAGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="11f11fs"
/clone_lib="Fusarium sporotrichioides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1317 GGATAAGGAGTGGACCAAGTATGCGCAGTACGTTGGTTAG 1356
                                                                                                                                                                                                                                                                                               organism="Fusarium sporotrichioides"
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/strain="Tri 10"
/db_xref="taxon:5514"
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les 371; Conservative
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JOURNAL

TITLE

AUTHORS

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14c09fs.rl Fusarium sporotrichioides Tri 10 overexpressed cDN
library Fusarium sporotrichioides cDNA clone 14c09fs 5', mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: T3
High quality sequence stop: 476.
Location/Qualifiers
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                                                                                                            Fusarium sporotrichioides
Fusarium sporotrichioides
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/strain="Tri 10"
                                                                           GI:14665687
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Best Local Similarity 81.0%;
Matches 324; Conservative
                                                                             BI192008.1
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     DEFINITION
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JOURNAL
COMMENT
                                                          ACCESSION
                                                                             VERSION KEYWORDS
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                                                                                                                                                                                                             AUTHORS
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                                                                                                                  SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pBlueScript SK-; Site_1: EcoR1; Site_2: Xho1; 5' end of cDNA cloned into EcoR1 site of pBluescript is 3' end of cDNA cloned into Xho1 site of pBluescript" is 129 c 111 g 125 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGAGCTTGATGTACTTTATGCCCAAGAGCCTGATGGCGAGTTCTGTGCGGCGCTTTCTC 1285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="13b10fs"
/clone lib="Fusarium sporotrichioides Tri 10 overexpressed
cDNA library"
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       Beremand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   926 ITCAAAACATGACCTACCACAACTCGACCATCGGCGAAATCGCCAACGAGTCACTCGGCG 985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 ACTITICACTITICACTICACTIAAGCCTCACACACACAACAACACCTITICAACCTITICA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62
                                                                                                                                                                                                                              Contact Dr. Marian Beremand regarding clone availability Included is the best homolog from a blastx search of Genbank nr 04-09-01 745 4e-79 gi|4378882|gb|AAD197 (AF127176) trichothecene3-0-acetyltransfer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1046 GICTCGCGACGIACCIGCACAACAACCCCGACAAGICCAACGIAICCCTGACGCTGAIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTCAAAACATGACCTACCATGACTCGACGTCGCCGAAATCGCCAACGAACCTTGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                            Unpublished
Other ESTS: 13b10fs.r1
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Copartment of Chemistry and Blochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Fax: 405 325 4912
       Tag,A., Peplow,A., Lai,H., Kupfer,C., Peterson,A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 12; Length 481;
           Ren,Q., Tag,A., Peplow,A., Lai,H., Kupfer,C., Peters
,M. and Roe,B.
Analysis of a Fusarium sporotrichioides EST database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                organism="Fusarium sporotrichioides"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 296.6; DB 1:
Pred. No. 2.2e-73;
0; Mismatches 84;
                                                                                                                                                                                                                                                                                                        Seg primer: M13-20
High quality sequence stop: 340.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                          db_xref="taxon:5514"
                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/strain="Tri 10"
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                                                                                                                                                                                                                 Email: broe@ou.edu
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Best Local Similarity
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Matches

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d à

BASE COUNT ORIGIN

FEATURES

EST 10-JUL-2001

linear

mRNA

514 bp

BI192008

RESULT 8 BI192008 LOCUS

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1 (bases 1 to 514)
Ren,Q., Tag,A., Peplow,A., Lai,H., Kupfer,C., Peterson,A., Beremand,M. and Roe,B.
Analysis of a Fusarium sporotrichioides EST database
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/clone="14c09fs"
/clone_lib="Fusarium sporotrichioides Tri 10 overexpressed
cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pBlueScript SK-; Site 1: EcoR1; Site 2:
XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript; 3' end of cDNA cloned into XhoI site of pBluescript"
162 c 112 g 105 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      183 AGCCGAGGGCATTAGCGAGGGAACACAGGAACTTCCTTTATCGTCCCTTTTGAGGACGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            295 GACCGAGGGCATCAGCGAAGGAAACACAGGAACTTCCAAGATCATTCCATATGAGGAGAC
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Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Hypocreomycetidae, Hypocreales, mitosporic Hypocreales, Fusari
                                                                                                                                                                                                                                                                                                                                                                                           Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Pax: 405 325 7762
Email: broe@ou.edu
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The bases I to 448)

Ren, O., Tag, A., Peplow, A., Lai, H., Kupfer, C., Peterson, A., Beremand, M. and Roe, B.

Analysis of a Fusarium sporotrichioides EST database
Unpublished
Contact: Burce A. Roe, University of Oklahoma, broe@ou.edu
Advanced Center for Genome Technology, University of Oklahoma
Advanced Center for Genome Technology, University of Oklahoma
620 parrington Oyal, Norman, OK 73019, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="o4c12fs"
/clone lib="Fusarium sporotrichioides Tri 10 overexpressed
cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: pBlueScript SK-; Site_1: EcoRI; Site_2: XhoI; S' end of cDMA cloned into EcoRI site of pBluescript i 3' end of cDMA cloned into XhoI site of pBluescript" i 126 c 101 g 114 t
                                                                                                                                                                                                                                                                                                               EST 10-JUL-2001
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Contact Dr. Marian Beremand regarding clone availability Included
is the best homolog from a blastx search of Genbank nr 04-09-01
694 4e-73 gi|4378882|gb|AAD197 (AF127176)
trichothecene3-0-acetyltransfer
                                                              298 TITCATTCACTCCCAAGGCCCTCTCGGAGCTGAAAGACGCAGCCACAAAAGACTCTTGACG
                               TCACATTCAGCCCCAAGGCCATGTCAGAGCTCAAGGATGCTGCTACCAAGACTCTTGACG
                                                                                                                                                                                                                                                                                                  BI201068 448 bp mRNA linear EST 10-JUL-04612fs.fl Fusarium sporotrichioides Tri 10 overexpressed cDNA library Fusarium sporotrichioides cDNA clone 04612fs 3', mRNA
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Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
                                                                                                                                                              761 CATCAACAAAGTTCGTGTCGACTGACGATGCTCTTTCGGCGTTCATCTGGAAAT
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/strain="Tri 10"
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Fax: 405 325 7762
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Ren, O., Tag, A., Peplow, A., Lai, H., Kupfer, C., Peterson, A., Beremand, M. and Roe, B.
Unpublished
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/clone="b2604fs"
/clone_lib="Pusarium sporotrichioides Tri 10 overexpressed
cDNA_library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: broe@ou.edu
Contact Dr. Marian Beremand regarding clone availability Included
is the best homolog from a blastx search of Genbank nr 04-09-01
591 4e-61 gi|4378882|gb|AAD197 (AF127176)
trichothecene3-0-acetyltransfer
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Hypocreomycetidae, Hypocreales, mitosporic Hypocreales, Fusarium.
                                                                                                                                            b2d04fs.rl Fusarium sporotrichioides Tri 10 overexpressed cDNA
library Fusarium sporotrichioides cDNA clone b2d04fs 5', mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AGCCTGTGTTGCTATTGCAGCTCAACTTCATTAAGGGCGGACTCATTCTCACCGTCAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        461 GACAGCACGCTGCTATGGATATGGTAGGCCAAGATGCGGTGATCCGTCTACTCTCCAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GACAACATGGTGCTATGGACATGACAGGACAAGATGCAATTATTCGTCTTCTCCCAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           521 CGTGCCGTAACGACCCATTCACCGAAGAAGAAATGACGGCCATGAACCTCGATCGCAAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Other_ESTS: b2d04fs.fl
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry buiversity of Oklahoma
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Pax: 405 325 7762
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475 ATTAGCTATCGGACCTGGCAATGGCCCCAACGACCGGAAG 514
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/strain="Tri 10"
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/mol_type="mRNA"
/strain="Tri 10"
/db_xref="taxon:5514"
/clone="b2d04fs"
/clone lib="Fusarium sporotrichioides Tri 10 overexpressed
cDNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                            303 GAGAAAGGCGGGATACCCTATGGCGATGTTTGACGAGAACATCATCGCGCCCAAGGAAGAC 362
                                                                                          246 ccirchdealadactaralactecriciteralactriceardachidachidachidaeana
                                                                                                                                                                                                                               306 GACCGAGGCATCAGCGAAGGAACAAGGAACTTCCAAGATCATCCATATGAGGAGAC 365
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Contact Dr. Marian Beremand regarding clone availability Included
is the best homolog from a blastx search of Genbank nr 04-09-01
655 Se-70 gpl 4378882 gpl AAD197 (AF127176)
trichothecene3-0-acetyltransfer
Seq primer: M13-20
High quality sequence stop: 257.
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Ren,Q., Tag,A., Peplow,A., Lai,H., Kupfer,C., Peterson,A., Berema,M. and Roe,B.
Analysis of a Fusarium sporotrichioldes EST database
                                                                                                                                                                                                                                                                                                       243 TCCTCGTGTTGTAGTGAAAGACCTCCGCGATGATCCTTCAGCGCCCACGATCGAGGGTAT
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b2d04fs.fl Fusarium sporotrichioides Tri 10 overexpressed cDNA
library Fusarium sporotrichioides cDNA clone b2d04fs 3', mRNA
                                                                                                                                                                     183 AGCCGAGGGCATTAGCGAGGGAAACACAGGAACTTCCTTTATCGTCCCTTTTGAGGACGT
                                CTTCGAGCAAGGTCTTAAGCGCTTCTCCGAAGCCGTCCCATGGGTCGCAGGCCAGGTCAA
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Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 445 325 4912
Fax: 445 325 7762
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/organism="Fusarium sporotrichioides"
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Fusarium sporotrichioides
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BI187780.1 GI:14661459
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1. (Dases 1 to 518)

Ren, Q., Tag, A., Peplow, A., Lai, H., Kupfer, C., Peterson, A., Beremand, M. and Roe, B.

Analysis of a Fusarium sporotrichioides EST database Umpublished
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/clone lib="Fusarium sporotrichioides Tri 10 overexpressed
cDNA library"
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14b10fs.rl Fusarium sporotrichioides Tri 10 overexpressed CDNA library Fusarium sporotrichioides CDNA clone 14b10fs 5', mRNA
                                                                                                            GACTGTGAGACGCCCAATCTTTGAGCCTGTTGAGAGCTTGATGTACTTTATGCCCCAAGAA 1253
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Contact br. Marian Beremand regarding clone availability Included
is the best homolog from a blastx search of Genbank nr 04-09-01
712 3e-75 gi |4378882 |gb|AAD197 (AF127176)
trichothecene3-0-acetyltransfer
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TICCTGGGCCAAGGTGGGATGCTGGGGAGTATGACTTTGGGTTTGGACTGGGTAAGCCTGA
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Fax: 405 325 7762
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/mol_type="mRNA"
/strain="Tri 10"
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Pred. No. 1.2e-66;
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0; Mismatches
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Location/Qualifiers
1. .518
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Fusarium sporotrichioides
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BI191997.1 GI:14665676
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Best Local Similarity 80.9%;
Matches 318; Conservative (
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/mol type="mRNA"
/strain="Tri 10"
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75;
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Seq primer: M13-20
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High quality sequence stop: 2
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80.2%;
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Matches 316; Conservative
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ACTCGACCATCGGCGAAATCGCCAACGAGTCACTCGGCGCAACAGCATCACGCCTTCGTT 1006
                                                                                                                    CAGAACTCGACCCGGGGGGGCATGCGCCAGCGAACAAGAGGTCTCGCGGACGTACCTGCACA 1066
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1 (bases 1 to 392)
Ren, Q., Tag, A., Peplow, A., Lai, H., Kupfer, C., Peterson, A., Beremand, M. and Roe, B.
Analysis of a Fusarium sporotrichioides EST database
Unpublished
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/clone lib="Fusarium sporotrichioides Tri 10 overexpressed
cDNA library"
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                                                       454 ACTCGACGTCGCCGAAATCGCCAACGA-ACCCTTGGCGCAACAGCATCACGCCTGCGCT
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Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
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Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
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High quality sequence stop: 361.
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/strain="Tri 10"
/db_xref="taxon:5514"
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Fusarium sporotrichioides
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Fax: 405 325 7762
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Contact Dr. Marian Beremand regarding clone availability Included
is the best homolog from a blastx search of Genbank nr 04-09-01
652 3e-68 gi|4378882|gb|AAD197 (AF127176)
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Hypocreomycetidae, Hypocreales, mitosporic Hypocreales, Fusarium.
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Gaps
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Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Fat: 405 325 4912
Fax: 405 325 7762
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1 (bases 1 to 490)

Ren, O., Tag, A., Peplow, A., Lai, H., Kupfer, C., Peterson, A., Beremand, M. and Roe, B.

Analysis of a Fusarium sporotrichioides EST database
Unpublished
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Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
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                                                                                                                                                                                             DB 12; Length 423;
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Pred. No. 1.7e-61;
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Best Local Similarity 79.6%;
Matches 301; Conservative
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Fax: 405 325 7762
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/note="Vector: pBlueScript 5K-; Site 1: EcoR1; Site 2:
XhoI; 5' end of cDNA cloned into EcoR1 site of pBluescript; 3' end of cDNA cloned into XhoI site of pBluescript"
153 c 104 g 103 t 1 others
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                                                                                                                                                                                                                                                                                                                                                                      Length 490;
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Location/Qualifiers
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ilarity 81.1%;
Conservative
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7, 2004, 21:46:44; Search time 530 Seconds (without alignments) 9424.540 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                               2449703 seqs, 1841816367 residues
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| 1000 | Description | Segmence 5. Appli | | 1 | Segmence 10. Appl | 7 | 276 | | | | | Segmence 24. April | | Semience 136 Ann | | 31187 |
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| * Query Match | | 100.0 | 67.5 | 67.5 | 67.5 | 18.4 | 2.9 | 2.6 | 2.6 | 2.6 | 2.6 | 2.6 | 2.6 | 2.6 | 5.6 | 2.6 |
| Score | | 1356 | 915.6 | 915.6 | 915.6 | 249.8 | 39.2 | 35.8 | 35.4 | 35.2 | 35.2 | 35 | 35 | 35 | 34.6 | 34.6 |
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| 8, A | 7. A | 8. A | 3. A | 19650, A | . Ap | Appl | Appl | App | Appl | Appl | Appl | Appl | Appl | Appl | Appl | Appl | Appl | Appl | Appl | Appl | Appl | Appl | App] | Appl | Appl | Appl | Appl | Appl | Appl |
|------------------|------------------|------------------|---------------------|-----------|--------------------|----------|----------|-------------|----------|------------------|----------|------------------|------------------|----------|-----------|----------|----------|------------------|----------|----------|------|------------------|--------|----------|-----------|----------|----------|---------|------------------|
| 3118 | 3118 | 3118 | 4653 | 1965 | 2148 | 30. | | 9 | | 10 | | 10, | | | | | | 10. | | | | | | | | | | 70. | |
| Sequence | Sequence | Sequence | Seguence | Sequence | Sequence | Sequence | Sequence | Seguence | Sequence | Seguence | Sequence | Sequence | Sequence | Sequence | Segmence | Sequence | Sequence | Sequence | Sequence | Sequence | | Sequence | | Sequence | | Sequence | a | | |
| -10-027-632-3118 | -10-027-632-3118 | -10-027-632-3118 | US-10-369-493-46533 | 10-242-53 | US-09-880-107-2148 | 60 | 10 | 10-240-965- | _ | US-10-141-761-10 | Ĩ. | US-10-158-790-10 | US-10-137-871-10 | | $\vec{-}$ | | ÷ | US-10-141-759-10 | 큐 | -10-14 | _ | US-10-141-761-70 | LO-142 | _ | -10 - 137 | 10-140 | -10 - 14 | 10 - 14 | US-10-141-756-70 |
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ALIGNMENTS

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61 ACCCAAATCAGTCTCCTCTACCCCGTCTCTGATTCCTCTCAATATCCCACTATTGTCAGC 120
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                                                                                                                                    APPLICANT: Peters, C.
APPLICANT: Rendra, D.
APPLICANT: Reindra, D.
APPLICANT: Reindras, J.
APPLICANT: Reindras, J.
APPLICANT: Dill-Mackey, R.
TITLE OF INVENTION: Transgenic Plant and Methods
TITLE OF INVENTION: Transgenic Plant and Methods
CURRENT APPLICATION NUMBER: US/10/074,279
CURRENT FILING DATE: 2002-02-12
PRIOR PELLICATION NUMBER: US/09/538,414
PRIOR PILLING DATE: 2000-03-29
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100.0%; Pred. No. 0;
iive 0; Mismatches
                 Sequence 5, Application US/10074279
Publication No. US20020162136A1
GENERAL INFORMATION:
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US-10-074-279-5
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 1356
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Best Local Similarity 100.
Matches 1356; Conservative
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US-10-074-279-5
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| Db 1201 AGAGGCCAATCTTTGAGGCTTGATGTACTTTATGCCCAAGAAGCCTGAT 1260 Qy 1261 GGCGAGTTCTGTGCGCGCTTTCTCTGAGGATATGGACTGTTGAGGGTT 1320 Db 1261 GGCGAGTTCTGTGCGCGCTTTCTCTGAGGATATGGACTGAGGCGAT 1320 Db 1321 AAGGAGTTCTGTGCGCGCTTTCTCTGAGGATATGGACCGATTGAAGGCGAT 1320 Qy 1321 AAGGAGTGCACCAAGTATGCGCAGTACGTTGGTTAG 1356 Db 1321 AAGGAGTGGACCAAGTATGCGCAGTACGTTAG 1356 Db 1321 AAGGAGTGGACCAAGTATGCGCAGTACGTTAG 1356 | RESULT 2 US-10-074-279-1 ; Sequence 1, Application US/10074279 ; Publication No. US20020162136A1 ; APPLICANT: Hohn, T. ; APPLICANT: Salmeron, J. ; APPLICANT: Kendra, D. ; APPLICANT: Reinders, C. ; APPLICANT: Reinders, J. | LE OF INVENTION: Training of the property of t | sarium sporotrich 67.5%; | SCHOOL OF THE STATE OF THE STAT | 183 | 303 GAGAAAGGGGGATACCCTATGGCGATGTTTGACGAGAACATCATCGCGCCAAGGAAGAC 303 GAGAAAGGCGGGTTTCCTTTGACGATGTTTTGACGAGACATCATCGCGCCAAGGAAGAC 363 GTTACCTATTGGACTTGGTCTCGTCGACGACGTCCTCGAGGAAGAC 363 GTTACCTATTGGACTTGGTCCTGGTCCCGAAAGCCTGTAATTCTATTGCAGT 396 ATTAGGTACTGGTACTGGTCCCCAAAGCCTGTAATTCTATTGCAGCT 423 CAACTTCATCAAGGCGGAATGGCCCCAACGACGACGAGCCTGTATTGCAGTT 456 CAACTTCATCAAGGCGGACTCATCTCCACCTCTCAACGACACAGCAGGTGCTATGGATAT 456 CAACTTCATTAAGGCGGGACTCATTCTCCACCGTCAACGGACAACATGGTGCTATGGATAT |
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| 121 ACCTTCGAGGAGGTCTTAAGGGCTTCCCGAAGGTCCATGGGTCGCAGGCCAGGTC 180 | | CATTC CATTC I TTGAA | GGTGGT GGTGGT \AGGCC | 721 ATGTCAGAGCTCAAGGATGCTCACCAAGACTCTTGACGCATCAACAACATGGTGTGG 780 721 ATGTCAGAGGATGCTGCTACCAGACTCTTGACGATCAACAACATGGTGTGG 780 721 ATGTCAGAGGATGCTCTTCGCTACCAGACTCTTGAGGATCGAACATCGTGTGG 780 781 ACTGACGATGCTCTTTCGGCGTTCATCTGGAAATCGGCCTCTCGCGTGCGT | | 1021 GCGAGCATGCGCCAGCGAACAAGAGTCTCGCGAGCTACCTGCAACAACCCCGACAAG 1080 1021 GCGAGCATGCGCCAGCGACCAGCGACCCGGACAAG 1080 1021 GCGAGCATGCGCCAGCGACCAGCACCACCACCACCACCACAAG 1080 1081 TCCAACGTATCCCTGACGGCTGATGCGGACCCATCATGCTGCTGATTCTTGG 1140 1081 TCCAACGTATCCCTGACGGCTGATGCGGACCCATCTACCAGCGTCATGCTGAGTTCTTGG 1140 1141 GCCAAGGTGGACTCTGGGATTACGACTTTGGGCTCGGACTGGGTAAGCCCGAGATTCTTGG 1200 1141 GCCAAGGTGGGACTCTGGGATTACGACTTTGGGCTCGGACTGGGTAAGCCCGAGACTGTG 1200 1141 GCCAAGGTGGGACTCTGGGATTACGACTTTGGGCTCGGACTGGGTAAGCCCGAGACTGTG 1200 1201 AGACGGCCAATCTTTGAGCCTGTTGAGACTTTATGCCCCAAGAAGCCTGAT 1260 |

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LENGTH: 12949

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APPLICANT: Dill-Mackey, R.
TITLE OF INVENTION: Transgenic Plant and Methods;
FILE REFERENCE: sequencelist
CURRENT APPLICATION NUMBER: US/10/074,279
CURRENT FILING DATE: 2002-02-12;
PRIOR APPLICATION NUMBER: US/09/538,414
PRIOR FILING DATE: 2000-03-29
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 11
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Pred. No. 4.7e-306;
0; Mismatches 264;
                                                        Query Match 67.5%;
Best Local Similarity 80.3%;
Matches 1087; Conservative
; TYPE: DNA
; ORGANISM: Plasmid
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Sequence 11, Application US/10074279 Publication No. US20020162136A1 GENERAL INFORMATION:

US-10-074-279-11

APPLICANT: Hohn, T.
APPLICANT: Salmeron, J.
APPLICANT: Peters, C.
APPLICANT: Kenders, D.
APPLICANT: Reinders, J.
APPLICANT: Kuznia, R.

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50 GICITITIGACATAGAGCICGACATCATCGGCCAGCAACCGCCICITCTTTCAATCTACAC 109
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                                                                CGATGGCTCTGCACCTACCGAGTTCTGCCGTGCTGTTGATGCTCGACCGGCAATGGGTGT
                                                                                                                     12118 GGATGCTTCCACACCTACTGAATTCTGCCGCGCTGTCGACATGCGGGGCCCAATGGGCGT
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US-1U-0/4-2/9-1U

Publication No. US20020162136A1

GENERAL INFORMATION:

APPLICANT: Bolneron, J.

APPLICANT: Redras, C.

APPLICANT: Reinders, J.

APPLICANT: Reinders, J.

APPLICANT: Reinders, J.

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APPLICANT: Reinders, J.

APPLICANT: Reinders, J.

APPLICANT: Ringers, Ed.

APPLICANT: Ringers: US.

APPLICANT: Dill-Mackey, R.

TITLE OF INVENTION: Transgenic Plant and Methods

FILE REFERENCE: sequencelist

CURRENT APPLICATION NUMBER: US/09/538,414

PRIOR PILING DATE: 2002-02-12

PRIOR PILING DATE: 2000-03-29

NUMBER OF SEQ ID NOS: 11

SOSTWARE PALENTIN Ver. 2.0

SEQ ID NO 10
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Best Local Similarity
Matches 1087; Conserv
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Publication No. US20030233675A1
GENERAL INFORMATION:
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                                          AAGACCTCGCTTTGAACCTTTTGAGAGTTTTGATGTACTTTTATGCCCAAGAAGCCTGGTGG
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               CAAGGTGGGACTCTGGGATTACGACTTTGGGCTCGGACTGGGTAAGCCCGAGAC
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Pred. No. 2.4e-75;
); Mismatches 622; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Hohn, T.
APPLICANT: Balmeron, J.
APPLICANT: Beters, C.
APPLICANT: Kendra, D.
APPLICANT: Kendra, D.
APPLICANT: Kendra, R.
APPLICANT: Karnia, R.
APPLICANT: Kuznia, R.
TITLE OF INVENTION: Transgenic Plant and Methods
FILE REFERENCE: sequencelist
CURRENT APPLICATION NUMBER: US/10/074,279
CURRENT APPLICATION NUMBER: US/09/538,414
PRIOR APPLICATION NUMBER: US/09/538,414
PRIOR FILING DATE: 2000-03-29
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                           GGAGTGGACCAAGTATGCGCAGTACGTTAG 1356
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Publication No. US20020162136A1
GENERAL INFORMATION:
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Sequence 37751, Application US/10369493

Sequence 37751, Application No. US2003023367BA1

GENERAL INFORMATION:

APPLICANT: Goo, Yongweir

APPLICANT: Glodman, Barry S.

APPLICANT: Glodman, Barry S.

APPLICANT: Chen, Xianfeng

TITLE OF INVENTION: EXPRESSION OF MICROBIAL EROTEINS IN PLANTS FOR PRODUCTION OF

TITLE OF INVENTION: EARNESSION OF MICROBIAL ENOTEINS IN PLANTS WITH IMPROVED PROPERTIES

TITLE OF INVENTION: EARNESSION OF MICROBIAL ENOTEINS IN PLANTS WITH IMPROVED PROPERTIES

TITLE OF INVENTION TOWNER: US/10/369,493

CURRENT APPLICATION NUMBER: US 60/360,039

PRIOR PRILING DATE: 2003-02-21

NUMBER OF SEQ ID NOS: 47374

TENERAL PARTICES OF MICROBIAL ENOTEINS IN UNBER OF SEQ ID NOS: 47374
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Pred. No. 0.89;
0; Mismatches 51; Indels 0;
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NUMBER OF SEQ ID NOS: 612
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Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 352, Application US/10184644 Publication No. US20030044930A1 GENERAL INFORMATION:
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Best Local Similarity 56.4%;
Matches 66; Conservative
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Gurney, Austin L
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Watanabe, Colin
Wood, William I.
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US-10-184-644-352
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LENGTH: 837
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APPLICANT: Eroshkin, Carlos
APPLICANT: Zamudio, Carlos
TITLE OF INVENTION: IDENTIFICATION OF ESSENTIAL GENES OF CRYPTOCOCCUS NEOFORMANS AND
TITLE OF INVENTION: METHODS OF USE
FILE REFERENCE: 10182-021-999
CURRENT APPLICATION NUMBER: US/10/320,797
CURRENT APPLICATION NUMBER: 60/341,261
PRIOR FILING DATE: 2001-12-17
NUMBER OF SEQ ID NOS: 3361
SOFTWARE: Patentin version 3.1
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILLE REFERENCE: 38 10 (52052) B
FILLE REFERENCE: 2003-02-28
PRIOR APPLICATION NUMBER: US (0/360,039
PRIOR FILING DATE: 2002-02-21
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Pred. No. 0.038;
n: Mismatches 73;
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Pred. No. 0.66
0; Mismatches
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Publication No. US20040014955A1
GENERAL INFORMATION:
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ORGANISM: Neurospora crassa
US-10-369-493-27681
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Best Local Similarity 53.2%
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NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 27681
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Matches 76; Conserv
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1135 TCTTGGGCCAAGGTGGGACTCTGGGATTACGACTTTGGGCTCGGACTGGGTAAGCCCGAG 1194
              1015 GACCCCGCGAGCATGCGCCAGCGAACAAGGGTCTCGCGACGTACCTGCACAACAACCC 1074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Eaton, Dan L.
APPLICANT: Eaton, Dan L.
APPLICANT: Eaton, Dan L.
APPLICANT: Geritzen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Goddwski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SCRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDE ENCODING THE SAME
FILE REFERENCE: P3230R1C1
CURRENT APPLICATION NUMBER: US/10/063,685
CURRENT APPLICATION THE SOR-0-50-06
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 170
: SEG ID NO 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            525 CCGTAACGACCCATTCACCGAAGAGAAATGACGGCCATGAACCTCGATCGCAAGACGAT 584
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                                                         495 G.ACHTW.SDMA.GKTDCN.DCSGW.TTG.....GDYSH.C.A..G.YHTRHMC..AB
                                                                                                                                                                                                                                                                                                                                      375 MSNHD.KN.BDC..DTTA.TS..CHH.B.TGSYT.HGBACBHTKC.AHGASBCG.H.YA.
                                                                                                                                                   1075 GACAAGTCCAACGTATCCCTGACGCTGATGCGGACCCATCTACCAGCGTCATGCTGAGT
                                                                                                                                                                                              ..b.T..MH..GDCRCNH..HA..YTSG.SW....HBDTKB.TKBDYSAS..CN.S.G.
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l Similarity 7.4%; Pred. No. 0.56;
33; Conservative 142; Mismatches 268; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 24, Application US/10063685; Publication No. US20030180909A1; GENERAL INFORMATION:
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ORGANISM: Homo Sapien
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APPLICANT: ZIANG, ZERATED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REPERENCE: P34391C217
CURRENT APPLICATION NUMBER: US/10/184,634
CURRENT FILING DATE: 2002-06-28
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
                                                                                                    895 ATGGGTGTCTCGAACAACTACCCAGGCCTTCTTCAAAACATGACCTACCACAACTCGACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 352, Application US/10184634
Publication No. US20030068684A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Watanabe, Colin K.
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Smith, Victoria
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Goddard, Audrey
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Best Local Similarity
Matches 52; Conserv
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Sequence 136, Application US/10184634
Publication No. US20030068684A1
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.SBBSM.HHMS..SRM..K..SG
                                                                                                                                                                 Smith, Victoria
Watanabe, Colin K.
Wood, William I.
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                                                                                                                            Godowski, Paul J.
Gurney, Austin L.
                                                                                                                 Goddard, Audrey
                                                                                                   Desnoyers, Luc
                                                                       APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
                                                                                                                                                                                                          Zhang, Zemin
                                                                                                                                                                                                                                                                                                                                                    Homo Sapien
                                                                                                                                                       Pan, James
                                                          GENERAL INFORMATION:
                       JS-10-184-634-136/c
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Best Local S
Matches 33
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APPLICANT:
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ORGANISM:
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Pred. No. 0.56;
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                                      945 CAACTCGACCATCGGCGAAATCG 967
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                                                                                                                             Sequence 136, Application US/10184644 Publication No. US20030044930A1 GENERAL INFORMATION:
                                                      89 .SBBSM.HHMS..SRM..K..SG
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Best Local Similarity 7.4%;
Conservative 142;
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Wood, William I.
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Godowski, Paul J.
Gurney, Austin L.
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Smith, Victoria
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  : :: 149 RYM..B..HM.
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APPLICANT:
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C217
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                Length 556;
                                                                                                                                                                                                                                                                                                                                                                                   / Match 2.6%; Score 35; DB 15; Length 55
Local Similarity 7.4%; Pred. No. 0.56;
Les 33; Conservative 142; Mismatches 268; Indels
                                                                                                                                                     Palm
                                                                                                                                        Prior Application removed - See File Wrapper or
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 136
                                                                                     CURRENT APPLICATION NUMBER: US/10/184,634 CURRENT FILING DATE: 2002-06-28
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US-10-374-780A-932
Sequence 932, Application US/10374780A
Publication No. US20040019927A1
GENERAL INFORMATION:
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
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APPLICANT: Dubell III, Arnold T
APPLICANT: Pineda, Omalixa
APPLICANT: You, Guo-Liang
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
FILE REFERENCE: MBI-0047 CIP
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ilarity 50.3%; Pred. No. 0.67;
Conservative 0; Mismatches 84;
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CURRENT FILING DATE: 2003-02-25
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                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 09/837,944
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PRIOR APPLICATION NUMBER: 10/225,067
PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 10/225,068
                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 2001-04-18
APPLICATION NUMBER: 60/310,847
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APPLICATION NUMBER: 09/934,455
FILING DATE: 2001-08-22
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FILING DATE: 2001-11-19
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FILING DATE: 2002-06-14
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iechmann, Jose Luis
iang, Cai-Zhong
eard, Jacqueline E
                                                                                         Creelman, Robert A
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NUMBER OF SEQ ID NOS: 2906
SOFTWARE: PatentIn version 3.2
SEQ ID NO 932
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Best Local Similarity
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ORGANISM: Zea mays
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Pred. No. 1.1;
0; Mismatches 74; Indels 0;
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                                                                                    FRIOR APPLICATION NUMBER: US 60/198,676
FRIOR FILING DATE: 2000-04-20
FRIOR PELLING DATE: 2000-04-20
FRIOR FILING DATE: 2000-03-29
FRIOR FILING DATE: 2000-02-24
FRIOR APPLICATION NUMBER: US 60/185,218
FRIOR RILING DATE: 2090-11-23
FRIOR APPLICATION NUMBER: US 60/167,363
FRIOR FILING DATE: 1999-11-23
FRIOR PELLING DATE: 1999-10-28
FRIOR FILING DATE: 1999-08-28
FRIOR FILING DATE: 1999-08-28
FRIOR FILING DATE: 1999-08-28
FRIOR FILING DATE: 1999-08-38
FRIOR APPLICATION NUMBER: US 60/146,002
FRIOR FILING DATE: 1999-08-09
FRIOR APPLICATION NUMBER: US 60/146,002
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                                                                        FILLING DATE: 2000-07-12
APPLICATION NUMBER: US 60/198,676
                                      PRIOR APPLICATION NUMBER: US 60/218,006
2002-04-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 51.6
Matches 79; Conservative
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Job time : 532 secs
CURRENT FILING DATE:
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ORGANISM: Human
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,; Search time 94 Seconds (without alignments) 6367.186 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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1356
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Minimum DB seq length: 0
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Listing first 45 summaries

1: /cgm2_6/ptodata/1/ina/5A_COMB.seq:*
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3: /cgm2_6/ptodata/1/ina/6A_COMB.seq:*
5: /cgm2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgm2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgm2_6/ptodata/1/ina/backfiles1.seq:* Issued Patents NA:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| | Description | Sequence 5. Appli | ì | H | 10. | 7,7 | 0 | H | .09 | | | | | 1, App | ΄, | Ŋ | Sequence 13, Appl | æ | 12, | 8923 | | 9159, | 10. Ar | 1338 | 1222, | 1386. | 7, Apr | |
|-----------|---------------|-------------------|-----------------|------------------|------------------|-----------------|------------------|------------------|----------------------|----------------------|----------------------|----------------------|----------------------|------------------|------------------|------------------|-------------------|------------------|-------------------|---------------------|---------------------|---------------------|-------------------|---------------------|---------------------|---------------------|------------------|---------------------|
| SUMMARIES | ID | US-09-538-414-5 | US-09-538-414-1 | US-09-538-414-11 | US-09-538-414-10 | US-09-538-414-7 | US-09-103-840A-2 | US-09-103-840A-1 | US-09-252-991A-16032 | US-09-252-991A-16568 | US-09-252-991A-16144 | US-09-252-991A-15293 | US-09-252-991A-15438 | US-09-198-452A-1 | US-09-125-642C-9 | US-09-125-642C-2 | US-09-125-642C-13 | US-09-125-642C-8 | US-09-125-642C-12 | US-09-252-991A-8923 | US-09-252-991A-9072 | US-09-252-991A-9159 | US-09-699-266A-10 | US-09-252-991A-1338 | US-09-252-991A-1222 | US-09-252-991A-1386 | US-08-492-027A-7 | US-09-252-991A-6665 |
| | DB | 4, | 4 | 4 | 4 | 4 | m | ٣ | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4, | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | ~ | 4 |
| | Length | 1356 | 1403 | 12949 | Н | | 4 | 4411529 | 720 | 1074 | 2721 | 516 | 1614 | 1230025 | 1620 | 1740 | 1742 | 5515 | 5519 | 1482 | 1782 | 2121 | 1406 | 1482 | 1671 | 1917 | 2190 | 456 |
| ₩ | Query | 100.0 | 67.5 | 67.5 | 67.5 | 18.4 | 2.9 | 2.9 | 2.5 | 2.5 | 2.5 | 2.5 | 2.5 | 2.4 | 2,4 | 2.4 | 2.4 | 2.4 | 2.4 | 2.4 | 2.4 | 2.4 | 2.4 | 2.3 | 2.3 | | | 2.3 |
| | Score | 1356 | 915.6 | 915.6 | 915.6 | 249.8 | 6 | φ. | 34.2 | 4 | 34.2 | 33.4 | 33.4 | 32.8 | 32.4 | 32.4 | 32.4 | 32.4 | 32.4 | 32.2 | 32.2 | | 32 | 31.4 | 31.4 | 31.4 | 31.4 | 31.2 |
| | Result No. | 1 | 7 | Э | 4 | Ŋ | 9 | 7 | œ | თ ე | 10 | c 11 | 12 | c 13 | 14 | 15 | 16 | 17 | _ | c 19 | 20 | C) I | c 22 | 23 | c 24 | 25 | 26 | 27 |

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Query Match Best Local Similarity 100. Matches 1356; Conservative

) TYPE: DNA ; ORGANISM: Fusarium graminearum US-09-538-414-5

LENGIH: 1356

DB 4; Length 1356; Indels 61 ACCCAAATCAGTCTCTTTTAGCCCGTCTCTGATTCCTCTCAATATCCCACTATTGTCAGC 120

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121 ACCTTCGAGGAAGGTCTTAAGGGCTTCTCCCGAAGCCGTCCCATGGGTCGCAGGCCAGGTC 181 AAAGCCGAGGCATTAGCGAGGAAACACAGGAACTTCCTTTATCGTCCCTTTTGAGGAC 181 AAAGCCGAGGGCATTAGCGAGGGAACACAGGAACTTCCTTTATCGTCCCTTTTGAGGAC

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241 GTTCCTCGTGTTGTAGTGAAAGACCTCCGCGATGATCCTTCAGCGCCCCACGATCGAGGGT 241 GIICCICGIGIIGIAGIGAAAGACCICCGCGAIGAICCIIICAGCGCCCACGAICGAGGCI 301 ATGAGAAAGGCGGGATACCCTATGGCGATGTTTGACGAGAACATCATCGCGCCAAGGAAG 360

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                                                                                                                                 CTCGAACAACTACCCAGGCCTTCTTCAAAACATGACCTACCACAACTCGACCATCGGCGA
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APPLICANT: Salmeron, J.
APPLICANT: Salmeron, J.
APPLICANT: Rendra, D.
APPLICANT: Rendra, D.
APPLICANT: Reinders, J.
APPLICANT: Reinders, J.
APPLICANT: Reinders, J.
APPLICANT: Reinders, J.
APPLICANT: Bill-Mackey, R.
TITLE OF INVENTION: Transgenic Plant and Methods
FILE REFERENCE: sequencelist
CURRENT APPLICATION NUMBER: US/09/538,414
CURRENT APPLICATION NUMBER: US/09/538,414
CURRENT APPLICATION NUMBER: 2000-03-29
NUMBER OF SEQ ID NOS: 11
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Pred. No. 1.3e-281;
0; Mismatches 264;
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Patent No. 6346655
GENERAL INFORMATION:
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Best Local Similarity 80.3
Matches 1087; Conservative
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US-09-538-414-11
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LENGTH: 12949
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GGCTTTCAAGATACAGCTCGACACCTCGGCCAGCTACCAGGCCTCCTTTCGATCTACAC
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                                                                                                     CCAAATCAGTCTCCTCTGCCCCGTCTCTGATTCCTCTAATATCCCACTATTGTCAGCAC
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APPLICANT: FIREISCHAMA, Robert D.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: PURTER, Obn C.
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
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                                                   APPLICANT: Hohn, T.
APPLICANT: Hohn, T.
APPLICANT: Balmeron, J.
APPLICANT: Salmeron, J.
APPLICANT: Peters, C.
APPLICANT: Reinders, D.
APPLICANT: Reinders, J.
APPLICANT: Reinders, J.
APPLICANT: Reinders, J.
APPLICANT: Reinders, J.
FILE OF INVENTION: Transgenic Plant and Methods
CURRENT APPLICATION NUMBER: US/09/538,414
CURRENT FILING DATE: 2000-03-29
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 249.8; DB 4;
Pred. No. 1.5e-69;
0; Mismatches 622;
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; ORGANISM: Saccharomyces cerevisiae
US-09-538-414-7
Application US/09538414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18.4%;
51.9%;
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Matches 700; Conservative
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Sequence 7,
Patent No.
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; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; LENGTH: 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 16144, Application US/09252991A ; Patent No. 6551795
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ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                            Pseudomonas aeruginosa
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Best Local Similarity 53.3%;
Matches 72; Conservative
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Best Local Similarity
Matches 72; Conserv
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US-09-252-991A-16144
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ORGANISM:
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Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
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                                                                     956 TCGGCGAAATCGCCAACGAGTCACTCGGCGCAACAGCATCACGCCTTCGTTCAGAACTCG
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Pred. No. 1.3;
); Mismatches 102;
        Pred. No. 1.3;
0; Mismatches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
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) OTHER INFORMATION: H37Rv
US-09-103-840A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/09103840A Patent No. 6294328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: WHITE, OWEN R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, JOHN C.
TITLE OF INVENTION: TUBERCULOSIS
TITLE OF INVENTION: TUBERCULOSIS
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APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
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              49.8%;
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                                 Conservative
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Best Local Similarity
Matches 101; Conserv
            Best Local Similarity
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                                   Matches 101;
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Sequence 16568, Application US/09252991A
; Sequence 16568, Application US/09252991A
; Patent No. 6551795
; General INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA. FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1998-02-18
; PRIOR PILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
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                                                                                                                                                               244 TATGATGCTGGAAAGCCAGCAGGGCTGCTTCGGCATCTCGCCGAGAAGCT 303
                                                                                                                                                                                                                          534 CCCATTCACCGAAGAGGAAATGACGGCCATGAACCTCGATCGCAAGACGATAGTTCCTTA 593
                                                                                                                                                                                                                                                                           304 caccarcacercedaceaceacearecearedeareaceaeceaeceaecearerereere 363
                                                                                                              474 TATGGATATGGTAGGCCAAGATGCGGTGATCCGTCTACTCTCCAAGGCGTGCCGTAACGA
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  Length 720;
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                                                          Indels
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Score 34.2; DB
Pred. No. 0.74;
                                                       0; Mismatches
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GENERAL INFORMATION:
APPLICANT: Griffais, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prever
TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
                                                                  Sequence 11438, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEEC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               956 TCGGCGAAATCGCCAACGAGTCACTCGGCGCAACAGCATCACGCCTTCGTTCAGAACTCG 1015
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Pred. No. 2.1;
0; Mismatches 66; Indels 0;
                                                                                                                                                                                                                       FILE REFERENCE: 107196.136
CURRENT APPLICATION WUMBER: US/09/252,991A
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 15438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/198,452A
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OTHER INFORMATION: n=a or c or g or t
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OTHER INFORMATION: n=a or c or g or NAME/KEY: misc feature
LOCATION: (45001)..(60000)
OTHER INFORMATION: n=a or c or g or NAME/KEY: misc feature
LOCATION: (60001)..(75000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT FILLING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: (15001)..(30000)
OTHER INFORMATION: ni=a or c or
NAME/KEY: misc_feature
LOCATION: (30001)..(45000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 2.5%;
1 Similarity 52.5%;
73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (1) .. (15000)
OTHER INFORMATION: n=a or c
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                                                  US-09-252-991A-15438
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LENGTH: 1230025
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US-09-198-452A-1/c
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Best Local S
Matches 73
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APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

APPLICANT: MOLIBIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 15293

LENGTH: 516
                  APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1914 CACCATCACCTCGGACGAGATGAGTGCCATCAGCAACCAGGTCAGCCATGTCGCCACGTC 1973
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.5%; Score 34.2; DE llarity 53.3%; Pred. No. 1.5; Conservative 0; Mismatches
                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
LENGTH: 2721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-252-991A-15293/c; Sequence 15293, Application US/09252991A; Patent No. 6551795
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US-09-252-991A-16144
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Best Local Similarity
GENERAL, INFORMATION:
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71

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990 AGCATCACGCCTTCGTTCAGAACTCGACCCCGCGAGCATGCGCCAGCGAACAAGAGGTCT 1049
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                                                                                                                                                                                                                                                                           12 ccarccciriocriococcacrososacroscoricrorrerrerrecentration
                                                                                                                                                                                                                                870 CCGIGCTGTTGATGCTCGACCGGCAATGGGTGTCTCGAACAACTACCCAGGCCTTCTTCA
                                                                                                                                                                                                                                                                                                                         330 AAACATGACCTACCACAACTCGACCATCGGCGAAATCGCCAACGAGTCACTCGGCGCAAC
                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/09125642C
Sequence 2. Application US/09125642C
Patent No. 6365393
GENERAL INFORMATION
APPLICANT: BAYER AG
TITLE OF INVENTION: Parapoxviruses Which Contain Foreign DNA, a
Their Production and Their Use in Vaccines
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APPLICATION UNBER: US/09/125,642C
FILING DATE: 20-Aug-1998
PRIOR APPLICATION DATA:
                                                                                                                                  Length 1620;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4; Length 1740;
                                                                                                                                    Score 32.4; DB 4; Length 1 Pred. No. 4.3; 0; Mismatches 116; Indels
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                     ORGANISM: Parapox ovis
STRAIN: D1701 Proteinkinase-Gen F10L (Version2)
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1050 CGCGACGTACCTGCACAACAACCCCGACAAGTCCAACG 1087
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STRAIN: D1701- Proteinkinase-Gen(Version 1)
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       192 CAAGACGCCCAACTGCGAAGACGCCGACAACTCCGACG 229
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FILING DATE: 17-Feb-97
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Bayer Corporation
STREET: 100 Bayer Road
CITY: Pittsburgh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 1740 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                    Query Match 2.4%;
Best Local Similarity 46.8%;
Matches 102; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U.S.A.
ZIP: 15205-9741
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2
ORIGINAL SOURCE:
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Best Local Similarity
Matches 102; Conserv
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US-09-125-642C-9
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IITLE OF INVENTION: Parapoxviruses Which Contain Foreign DNA, a
IITLE OF INVENTION: Their Production and Their Use in Vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1230025,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
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COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37;
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APPLICATION NUMBER: US/09/125,642C
FILING DATE: 20-Aug-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP97/00729,
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 32.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Bayer Corporation
STREET: 100 Bayer Road
                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc feature
LOCATION: (900001)..(915000)
OTHER INFORMATION: n=a or c or g or t
                                                                                                                                                                                                                                                                                          NAME/KEY: misc feature
LOCATION: (87001)..(88500)
OTHER INFORMATION: n=a or c or g or
NAME/KEY: misc feature
LOCATION: (885001)..(90000)
OTHER INFORMATION: n=a or c or g or
or
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LENGTH: 1620 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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MOLECULE TYPE: DNA (genomic)
n=a or c or g
                   NAME/KEY: misc_feature
LOCATION: (810001)..(825000)
OTHER INFORMATION: n=a or c or NAME/KEY: misc_feature
LOCATION: (825001)..(840000)
OTHER INFORMATION: n=a or c or
                                                                                                                                                       NAME/KEY: misc feature
LOCATION: (840001)..(855000)
OTHER INFORMATION: n=a or c or
                                                                                                                                                                                                                      NAME/KEY: misc feature
LOCATION: (85501)..(87000)
OTHER INFORMATION: n=a or c or
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Pittsburgh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 59.8
Matches 55, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-125-642C-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
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